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Transmitted herewith for filing is the continuing patent application entitled *Robo: A Novel Family of Polypeptides and Nucleic Acids* under 37 CFR 1.78(a) of copending provisional application Serial No. 60/062,921 filed October 20, 1997, entitled *Robo: A Novel Family of Genes and Proteins*, both having the inventors: Corey S. Goodman, Thomas Kidd, Kevin J. Mitchell and Guy Tear, all of Berkeley, CA; 74 pages (including 2 Figures), 9 claims (2 independent); Paper copy of Sequence Listing(33p); CRF of Sequence Listing; return postcard. Atty Docket No: **B98-006**

In adherence with 37 CFR 1.821-1.825, this application is accompanied by a diskette containing SEQ ID NOS 01- 12 in computer readable form and a paper copy of the sequence information. The computer readable sequence listing was prepared through the use of the software program "PatentIn" provided by the Patent and Trademark Office. The paper copy and computer readable copy of the sequence listing are the same. The sequence data of the Sequence Listing are all contained in the Specification filed herewith.

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Robo: A Novel Family of Polypeptides and Nucleic Acids

Inventors: Corey S. Goodman, Thomas Kidd, Kevin J. Mitchell and Guy Tear

This application claims priority to US Provisional Application No. 60/062921 filed Oct 20, 1997 by Corey S. Goodman, Thomas Kidd, Kevin J. Mitchell, and Guy Tear and entitled *Robo: A Novel Family of Genes and Proteins.*

The research carried out in the subject application was supported in part by NIH grant NS18366. The government may have rights in any patent issuing on this application.

INTRODUCTION

Field of the Invention

The field of this invention is proteins involved in nerve cell guidance.

Background

Bilaterally symmetric nervous systems, such as those found in insects and vertebrates, have special midline structures that establish a partition between the two mirror image halves. Axons that link the two sides of the nervous system project toward and across the midline, forming axon commissures. These commissural axons project toward the midline, at least in part, by responding to long-range chemoattractants emanating from the midline. One important class of midline chemoattractants are the netrins (Serafini et al., 1994; Kennedy et al., 1994), guidance signals whose structure, function, and midline expression is evolutionarily conserved from nematodes and fruit flies to vertebrates (Hedgecock et al., 1990; Wadsworth et al., 1996; Mitchell et al., 1996; Harris et al., 1996). The attractive actions of netrins appear to be mediated by growth cone receptors of the DCC subfamily of the immunoglobulin (Ig) superfamily (Keino-Masu et al., 1996; Chan et al., 1996; Kolodziej et al., 1996).

The midline also provides important short-range guidance signals. This is best illustrated by considering the different classes of axon projections in the spinal cord of vertebrates or the nerve cord of insects. Although some growth cones extend away from the midline, most extend towards or along the midline during some segment of their trajectory. Certain classes of growth cones either extend towards the midline or longitudinally along it

and yet never cross it. Most growth cones (~90% in the Drosophila CNS), however, do cross the midline. After crossing, the majority of these growth cones turn to project longitudinally, growing along or near the midline. Interestingly, these axons never cross the midline again, despite navigating in the vicinity of other axons that continue to cross.

What midline signals and growth cone receptors control whether growth cones do or do not cross the midline? After crossing once, what mechanism prevents these growth cones from crossing again? Studies in the chick (Stoeckli and Landmesser, 1995; Stoeckli et al., 1997) and grasshopper (Myers and Bastiani, 1993) embryos have led to the suggestion that the midline contains a contact-mediated repellent, and that commissural growth cones must overcome this repellent to cross the midline. For example, this notion that the midline can be repulsive even to growth cones that cross it is supported by time-lapse imaging of the first commissural growth cone in the grasshopper embryo. On contacting the midline, this growth cone often abruptly retracts, although ultimately it overcomes the repulsion and crosses the midline.

One approach to find the genes encoding the components of such a midline guidance system is to screen for mutations in which either too many or too few axons cross the midline. Such a large-scale mutant screen was previously conducted in Drosophila and led to the identification of two key mutations: *commissureless* (*comm*) and *roundabout* (*robo*) (Seeger et al., 1993; reviewed by Tear et al., 1993). In *comm* mutant embryos, commissural growth cones initially orient toward the midline but then fail to cross it and instead recoil and extend on their own side. *comm* encodes a novel surface protein expressed on midline cells. As commissural growth cones contact and traverse the CNS midline, Comm protein is apparently transferred from midline cells to commissural axons (Tear et al., 1996). In *robo* mutant embryos, many growth cones that normally extend only on their own side instead now project across the midline, and axons that normally cross the midline only once instead appear to cross and recross multiple times (Seeger et al, 1993; Kidd et al., 1997). Double mutants of *comm* and *robo* display a *robo*-like phenotype.

Here we disclose the characterization of *robo* across animal species. *robo* encodes a new class of guidance receptor with 5 Ig domains, 3 fibronectin (FN) type III domains, a transmembrane domain, and a long cytoplasmic domain. Robo defines a new subfamily of Ig superfamily proteins that is highly conserved from fruit flies to mammals. The results of protein expression and transgenic rescue experiments indicate that Robo functions as the

gatekeeper controlling midline crossing and that Robo responds to an unknown midline repellent.

SUMMARY OF THE INVENTION

The invention provides methods and compositions relating to Robo1 and Robo2, collectively Robo) polypeptides, related nucleic acids, polypeptide domains thereof having Robo-specific structure and activity, and modulators of Robo function. Robo polypeptides can regulate cell, especially nerve cell, function and morphology. The polypeptides may be produced recombinantly from transformed host cells from the subject Robo polypeptide encoding nucleic acids or purified from mammalian cells. The invention provides isolated Robo hybridization probes and primers capable of specifically hybridizing with natural Robo genes, Robo-specific binding agents such as specific antibodies, and methods of making and using the subject compositions in diagnosis (e.g. genetic hybridization screens for Robo transcripts), therapy (e.g. Robo inhibitors to promote nerve cell growth) and in the biopharmaceutical industry (e.g. as immunogens, reagents for isolating Robo genes and polypeptides, reagents for screening chemical libraries for lead pharmacological agents, etc.).

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 Organization of the roundabout Genomic Locus

(A) Cosmid chromosome walk through the 58F/59A region of the 2nd chromosome. The position of deficiency breakpoints within the cosmids used are shown in the top two rows. Identified transcripts from the walk are shown below the cosmids. The 12-1 transcript corresponds to the *robo* gene; the direction of transcription is distal to proximal. The location of the 16kb XbaI genomic rescue fragment is indicated below.

(B) Position and size of introns within the *robo* transcript. Coding sequence is indicated by the thicker part of the line. Introns are represented by gaps. The transcript is shown 3'-5' to reflect its orientation in (A).

Figure 2 Structure of Robo Protein

Schematic of the structure of Drosophila Robo protein. The position of the Immunoglobulin (Ig), fibronectin (FN) and transmembrane (TM) domains and the amino acid substitution in *robo*^{6} are shown. Percent amino acid identity between Drosophila Robo 1 and Human Robo 1

is indicated for each domain.

DETAILED DESCRIPTION OF THE INVENTION

The nucleotide sequences of exemplary natural cDNAs encoding drosophila 1, drosophila 2, C. elegans, human 1, human 2 and mouse 1 Robo polypeptides are shown as SEQ ID NOS:1, 3, 5, 7, 9 and 11, respectively, and the full conceptual translates are shown as SEQ ID NOS:2, 4, 6, 8, 10 and 12. The Robo polypeptides of the invention include incomplete translates of SEQ ID NOS:1, 3, 5, 7, 9 and 11 and deletion mutants of SEQ ID NOS:2, 4, 6, 8, 10 and 12, which translates and deletion mutants have Robo-specific amino acid sequence, binding specificity or function. Preferred translates/deletion mutants comprise at least a 6, preferably at least an 8, more preferably at least a 32, most preferably at least a 64 residue domain of the translates. In a particular embodiment, the deletion mutants comprise one or more structural/functional Robo immunoglobulin, fibronectin or cytoplasmic motif domains described herein. For example, soluble forms of the disclosed Robo polypeptides which comprise one or more Robo IG domains, and especially fusions of two or more Robo IG domains, particularly fusions of IG#1 and #2, provide competitive inhibitors of Robo-mediated signaling. Exemplary such deletion mutants and recombined deletion mutant fusions include human Robo 1 (SEQ ID NO:8) residues 1-67; 68-167; 168-259; 260-350; 351-451; 1-167; 1-259; 1-350; 1-451; 68-259; 1-67 joined to 168-259; and 1-67 joined to 260-451.

Other deletion mutants provide Robo-specific antigens and/or immunogens, especially when coupled to carrier proteins as described below. Generic Robo-specific peptides are readily apparent as conserved regions in the aligned Robo polypeptide sequences of Table 1.

Table 1. Sequence Alignment of Robo Family Members: The complete amino acid alignment of the predicted Robo proteins encoded by *drosophila robo 1* (D1, SEQ ID NO:2) and Human *robo 1* (H1, SEQ ID NO:8) are shown. The extracellular domain of *C.elegans robo* (CE, SEQ ID NO:6; Sax-3; Zallen et al., 1997), the extracellular domain of *Drosophila robo 2* (D2, SEQ ID NO:4), and partial sequence of Human *robo 2* (H2, SEQ ID NO:10) are also aligned. The D2 sequence was predicted by the gene-finder program Grail. The position of immunoglobulin domains (Ig), fibronectin domains (FN), the transmembrane domain (TM), and conserved cytoplasmic motifs are indicated. The extracellular domain of rat *robo 1* is nearly identical to H1.

```
mH.............PMHpENHAIaRSTSTTNNPSrsRSSRMWLlpAWLLLVLVASNGLP   47 D1
m.FNRKTLlCTi.llVlQA.............vIrsFCEDASNlA.............   30 CE
mKWKHVPFlVMiSllSlSpNHLFLaQLIPDPEDvErG.NDHGTPIpTSDNDDNSLGYTGS   59 H1

        >IG #1
AVrGQYQSpriiehpTdlvvKknepatlnckVegKpEptiewfkdgepvStn..EKKshr  105 D1
     GENpriiehpMdTTvPknDpFtFncQaegNptptiQwfkdgRELKt...dTGshr      D2
........pViiehpIdVvvsRgSpatlncGaK.PStAKiTwykdgQpvItnkEQVNshr   81 CE
RLrQEDFPpriVehpSdlIvskgepatlnckaegRptptiewykGgeRvEtDkDdPRshr  119 H1

                                                >IG #2
VQFKDgAlffYriMQgkkeQ..dGgEywcvaknRVgQavsrHaslqIavlrddfrvepKd  163 D1
iMlpAgGlfflkvIhSrReS..dagTywcEakneFgVaRsrnaTlqvavlrdEfrLepAN      D2
iVlDTgslfLlkvNSgkNGKDSdagAyYcvaSneHgeVKsNEGslKLaMlrEdfrvRpRT  141 CE
MLlpSgslfflriVhgrkSRP.dEgVyVcvaRnYLgeavsHnaslEvaIlrddfrQNpSd  178 H1

trvaKgeTallecgppKgIpeptLIwIkdgVplddLKAmSFGASSrVrivdggnlLiSNv  223 D1
trvaQgeValmecgAprgSpepQiswrkNgQTlNL......VGNKririvdggnlAiQEA      D2
vQALGgeMavlecSpprgFpepVVswrkdDKElRI.QDmP.....rYTLHSDgnlIiDPv  195 CE
vMvaVgePavmecQpprgHpeptiswKkdgSpldd.......KDEri.TIRggKlMiTYT  230 H1

                                    >IG #3
EPIdEgNyKcIaQnLvgtresSYaKlIvQvkpYfMkepkdqVMLYgQTaTfHcSvggdpP  283 D1
rQsdDgRyqcvVKnVvgtresATaFlKvHvrpFLIRGpQnqtAVvgSsvVfQcrIggdpL      D2
DRsdSgTyqcvaNnmvgerVsNPaRlSvFekpKfEQepkdMtvDvgAAvLfDcrvTgdpQ  255 CE
rKsdAgKyVcvGTnmvgeresEVaElTvLerpSfVkRpSnLAvTvDDsaEfKcEARgdpV  290 H1

pKvlwkk..EEgnIpvsrA..........RiLHdEKslEiSNItpTdegTyvceaHnNvg  331 D1
pDvlwrrTASGgnmpLRKFSWLHSASGRVHVl.EdrslkLDDvtLEdmgeytceaDnAvg      D2
pQITwkr..KNEPmpvTra..........YiAKdNrGlRiERvQpSdegeyvcYaRnPAg  303 CE
pTvRwrk..DDgELpKsrY..........Ei.RddHTlkiRKvtAGdmgSytcVaEnMvg  337 H1

              >IG #4
QiSaRaSlIvhappNfTKrpSnKKvGlNgVvQLPcMaSgnpPpSvfwTkegVSTlMfpn.  388 D1
GiTaTGIltvhappKfvIrpKnqLvEIgDEvLfecQaNgHpRpTLYwsVegNSSllLpGy      D2
TLeasaHlRvqappSfQTkpAdqSvPAggtAtfecTLVgQpSpaYfwskegQqDllfpsy  363 CE
KAeasaTltvqEppHfvVkpRdqVvalgrtvtfQceaTgnpqpaIfwRRegsqnllf.sy  396 H1
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                    qIvaQgrtvtfPceTKgnpqpavfwQkegsqnllfpn.      H2

...SsHGrQYvAADgtlQitDvrqedegyyv.cSaFSvvDssTVrVFlQvSS..vD....  440 D1
RDGRMEVTLTPEGRSVlSiARFAredSgKVvTcNalnAvgsVSsrTVVSvDt..QF....      D2
VSADGRTK..vsptgtltiEEvrqVdegAyv.cAGMnSagsslskaAlKvttKAvTGNTP  420 CE
qpPQsSsrFsvsQtgdltitnvqrsdVgyyi.cqTlnvagsiITkaYlevtd..vIA...  450 H1
qpQQPNsrCsvsptgdltitnIqrsdAgyyi.cqalTvagsilAkaQlevtd..vLT...      H2

>IG #5
erpppiiQIgpAnqtlpKgsVaTlpcratgNpSpRiKwFHdgHAvQA.GNRYSi.iqG..  496 D1
eLpppiieqgpvnqtlpvKsIVvlpcrTLgTpvpQVswYLdgIpidVqEHERrNLsDA..      D2
AKpppTieHgHQnqtlMvgsSaIlpcQaSgKpTpGiswlRdgLpidITd..sri.sqHST  477 CE
drpppViRqgpvnqtVavdgtFvlScVatgSpvpTiLwRkdgVLvSTqd..sriK.qLeN  507 H1
drpppiiLqgpAnqtlavdgtaLcKcKatgDpLpViswlkEgFTFPGRd..PrATiq.eQ      H2

                                >FN #1
SslRVDdlq.lsdSgtytciasGeRgeTswAaTltveKpgs..TSLHraAdpstypAppg  553 D1
gAlTiSdlqrHEdEgLytcvasnRNgKsswsGylRLDTptNpNiKfFrapElstypgppg      D2
gslHiAdl.kKPdtgVytciaKneDgestwsaSltveDHtsN.AqfVrMpdpsNFpsSpT  535 CE
gvlqiR.YAklGdtgRytciasTPsgeatwsayIEvQeFgVp.VqPPrPTdpNLIpsAps  565 H1
gTlqiKNl.rIsdtgtytcvaTSSsgeaswsaVlDvTeSgAT.i..SKNYdlsDLpgpps      H2

TpKvLnvsrtsISlRwAKSqEKPGAVgpIi.gyTVeyfspdlQTgwIVAaHrvGDtQVti  612 D1
kpqMvEKGEnsvtlsw...TRSNKVggSSLVgyVieMfGKNETDgwVAvGTrvQNttFtQ      D2
QpIIvnvtDtEvElHw...NAPSTsgaGpitgyiiQyYspdlgQTwFNIPDYvAStEyRi  592 CE
kpEvtdvsrnTvtlsw...qpNLNsgaTp.tSyiieafsHASgSswqtvaENvktEtSAi  621 H1
kpqvtdvtKnsvtlsw...qpGTPGTLpA.SAyiieafsQSVSNswqtvaNHvkttLytV      H2

                        >FN #2
SglTpgtsyVflvraenTQgisvpsGLsNViktIEA....DfDAASANdlsAarT.llTg  667 D1
TglLpgVNyFfliraenSHgLsLpsPMsEpitVGTR....YfNS..gLdlsEarASllsg      D2
kglkpSHsyMfViraenEkgiGTpsVSsALvttSKPAAQVAlSDKNKMdMAIaEKRlTsE  652 CE
kglkpnAiylflvraAnAYgisDpsqIsDpvktQDV.....lPTSQgVdHKQVQRE.lGN  675 H1
RglRpntiylfMvraInPkV.svT.q                                     H2

KSvelIDasAinAsavrlEwMLHvSADEkyvegLRiHyK..DaSVPSAQYHSITvMDAsa  725 D1
DvvelSnasvVDstsMKlTwQI...INGkyvegFyVYArQLpNPLNTKyRMLTILNGGGa      D2
QLIKlEEVKTinstavrlFwKKR..KLEELiDgyyiKWrGPpRTNDNQyVN...vTSpsT  707 CE
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AvLHlHnPTvLSsssIEVHwT..vDQQSQyiQgyKiLyrPSGaNHGESDWLVFEvRTpAK  733 H1

                                >FN #3
esFvvGnlKkytKyeffLTpf...fETiegQpsnskTaltYedvpsappDNIQiGmYn..  780 D1
SsCTiTGlVQytLyeffIVpf...YKsVegKpsnsRIaRtledvpsEApYgMEALLln..      D2
eNYvvSnlMPFtnyeffVIpYHSGVHsiHgapsnsMDVltAeAPpsLppEDvRiRmlnL.  766 CE
NsVviPDlRkGVnyeIKARpf...fNEFQgaDsEIkFaKtleEApsappQgvTVSKNDGN  790 H1

QtaGWvRwTpppSQHHngNlYgykiEVSAgnTM.....KVlAnMtLnaTtTsvLlNnltt  835 D1
SSaVFLKwkapELKDRHgVlLNyH.vivRgIDtAHNFSRIlTnVtIdaASPTLvlAnltE      D2
.tTLRIswkapKAdGIngIlKgFQiviv.gQAPNNNR.....nItTnERAAsvTlFHlVt  819 CE
GtaILvswQpppEdTQngMVQEykV.WCLgnEtR.....YHInKtVdGStFsvvIPFlVP  844 H1

                        <
gAVysvrLNSFtKagDgpysKpISlFMdpTHHVHPpRAHPsGTHDGRHEGqDLTYHNNgN  895 D1
gVMyTvGvaaGNnagvgpyCVpATlRldpITKRLDpFINQRDHVND.............      D2
gMTyKIrvAARSnGgvgv..........ShgTSEVIMNqDTlEKHL.AAQqENESFLYgL  868 CE
gIRysvEvaaStGagSgvKsEpQFIQldAhgNPVSpEDqVslAQQI.............  890 H1

                    >              TM              <
iPPGDINPTTHKKTTdYlSGpwLMViVCiVlLvlVisAAIsM.vyFkrkhQmTKElGHLS  954 D1
.................vlTqpwFIiiLgAilavlMLs..fGAMvFVkrkhMm..MkQsAL      D2
iNK.............SHVpVIViVaILiIFvViiIAY.CYwRNS.rNSD...gkDRSF  909 CE
.............SdvVKqp..AFiagiGAaCWiiLMVfsIwLyRHrkKR..NglTsTY  932 H1

VVSDNEIT.....................AlniNSKESL.wIDHHRGwRTADTDKD..  988 D1
AGIRKVPSFTFTPTVTYQRGGEAVSSGGRPGLlniSEPAAQPwLAD..TwPNTGNNHNDC  990 H1

........SgLsEsKlLSHVNSSQ..SnynnS..........DGGtDyAEvd....TRNL 1024 D1
SISCCTAGNgNsDsNlTTYSRPADCIAnynnQLDNKQTNLMLPEStVyGDvdLSNKINEM 1050 H1

                CYTOPLASMIC MOTIF #1
TtfYNCR.......KSPDNptpyattMIiGTS........sSETCTkT.TSISADkDSGT 1068 D1
KtfNSPNLKDGRFVNPSGQptpyattQLiQSNLSNNMNNGsGDSGEkHWKPLGQQkQEVA 1110 H1

HSPyS........DAFAGQVPAVpVV..KSNyLqYPVEP..................... 1097 D1
PVQyNIVEQNKLNKDYRANDTVPpTIPYNQSyDqNTGGSYNSSDRGSSTSGSQGHKKGAR 1170 H1
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CYTOPLASMIC MOTIF #2

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.........InwSEFlppppEhppp...sSTy......GyAqGSp.............. 1124 D1
TPKVPKQGGMnwADLlppppAhpppHSNsEEyNISVDESyDqEMpCPVPPARMYLQQDEL 1230 H1

..eSSRKSSKSAGSgISTNQSILNAsIHsSSSGGFsAWGVSPQYAVAcp.......... 1171 D1
EEeEDERGPTPPVRgAASSPAAVSYsHQsTATLTPsPQEELQPMLQDcpEETGHMQHQPD 1290 H1

...............pENVy...sNpl.....SAVAGGTQNRYQITPTNQHPPQl.... 1203 D1
RRRQPVSPPPPPRPISpPHTyGYIsGplVSDMDTDAPEEEEDEADMEVAKMQTRRlLLRG 1350 H1

....paY..............FATTGPGGAVPPNHLP.............faTQRHaa 1230 D1
LEQTpaSSVGDLESSVTGSMINGWGSASEEDNISSGRSSVSSSDGSFFTDADfaQAVAaa 1410 H1

SeyQaglNAar..............cAQSRACNsCdALATPSPmq............. 1261 D1
Aey.aglKVarRQMQDAAGRRHFHASQcPRPTSPVsTdSNMSAAVmqKTRPAKKLKHQPG 1469 H1
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CYTOPLASMIC MOTIF #3

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..........ppppvpVpEGWYQPVHPNSH.PMHpTS.SNHQIYQCSSECsDHSRSsQS 1307 D1
HLRRETYTDDLpppppvpPpAIKSPTAQSKTQLEVRpVVVPKLPSMDARTDRsSDRKGsSY 1529 H1

HKrQL..............QLEeHGSSAkQrgGHHRRrA.pVVQPCMESeN......ENM   D1
KGrEVLDGRQVVDMRTNPGDPREAQeQQNDGkGrgNKAAKrDLpPAKTHLIQeDILPYCRPTF   H1

LAEYEQrQYTsDCCNssrEGDTC.........SCSeGSCl..yAeAgePAPRQMTAKNT 1395 D1
PTSNNPrDPSsSSSMssrGSGSRQREQANVGRRNIAeMQVlGGy.eRgeDNNEELEETES 1651 H1
```

Exemplary such Robo specific immunogenic and/or antigenic peptides are shown in Table 2.

Table 2. Immunogenic Robo polypeptides eliciting Robo-specific rabbit polyclonal antibody: Robo polyeptide-KLH conjugates immunized per protocol described below.

Robo Polypetide, Sequence	Immunogenicity
SEQ ID NO:2, residues 68-77	+++
SEQ ID NO:2, residues 79-94	+++
SEQ ID NO:2, residues 95-103	+++
SEQ ID NO:2, residues 122-129	+++
SEQ ID NO:2, residues 165-176	+++

SEQ ID NO:2, residues 181-191	+++
SEQ ID NO:2, residues 193-204	+++
SEQ ID NO:2, residues 244-251	+++
SEQ ID NO:2, residues 274-290	+++
SEQ ID NO:2, residues 322-331	+++
SEQ ID NO:2, residues 339-347	+++
SEQ ID NO:2, residues 407-417	+++
SEQ ID NO:2, residues 441-451	+++
SEQ ID NO:2, residues 453-474	+++
SEQ ID NO:2, residues 502-516	+++
SEQ ID NO:2, residues 541-553	+++
SEQ ID NO:2, residues 617-629	+++

In addition, species-specific antigenic and/or immunogenic peptides are readily apparent as diverged extracellular or cytosolic regions in Table 1. Exemplary such human specific peptides are shown in Table 3.

Table 3. Immunogenic Robo polypeptides eliciting human Robo-specific rabbit polyclonal antibody: Robo polyeptide-KLH conjugates immunized per protocol described below (some antibodies show cross-reactivity with corresponding mouse/rat Robo polypeptides).

Robo Polypetide, Sequence	Immunogenicity
SEQ ID NO:8, residues 1-12	+++
SEQ ID NO:8, residues 18-28	+++
SEQ ID NO:8, residues 31-40	+++
SEQ ID NO:8, residues 45-65	+++
SEQ ID NO:8, residues 106-116	+++
SEQ ID NO:8, residues 137-145	+++
SEQ ID NO:8, residues 174-184	+++
SEQ ID NO:8, residues 214-230	+++
SEQ ID NO:8, residues 274-286	+++
SEQ ID NO:8, residues 314-324	+++
SEQ ID NO:8, residues 399-412	+++

SEQ ID NO:8, residues 496-507	+++
SEQ ID NO:8, residues 548-565	+++
SEQ ID NO:8, residues 599-611	+++
SEQ ID NO:8, residues 660-671	+++
SEQ ID NO:8, residues 717-730	+++
SEQ ID NO:8, residues 780-791	+++
SEQ ID NO:8, residues 835-847	+++
SEQ ID NO:8, residues 877-891	+++
SEQ ID NO:8, residues 930-942	+++
SEQ ID NO:8, residues 981-998	+++
SEQ ID NO:8, residues 1040-1051	+++
SEQ ID NO:8, residues 1080-1090	+++
SEQ ID NO:8, residues 1154-1168	+++
SEQ ID NO:8, residues 1215-1231	+++
SEQ ID NO:8, residues 1278-1302	+++
SEQ ID NO:8, residues 1378-1400	+++
SEQ ID NO:8, residues 1460-1469	+++
SEQ ID NO:8, residues 1497-1519	+++
SEQ ID NO:8, residues 1606-1626	+++
SEQ ID NO:8, residues 1639-1651	+++
SEQ ID NO:10, residues 5-16	+++
SEQ ID NO:10, residues 38-47	+++
SEQ ID NO:10, residues 83-94	+++
SEQ ID NO:10, residues 112-125	+++
SEQ ID NO:10, residues 168-180	+++
SEQ ID NO:10, residues 195-209	+++
SEQ ID NO:10, residues 222-235	+++
SEQ ID NO:10, residues 241-254	+++

In a particular embodiment, expressed sequence tags EST;yu23d11, Accession #H77734 and EST;yq76e12, Accession #H52936, as well as peptides conceptually encoded thereby, are not within the scope of the present invention (Tables 4 and 5). In a particular

embodiment, the subject Robo polypeptides exclude the corresponding regions of the disclosed natural human Robo I polypeptide, i.e. SEQ ID NO:8, residues 168-217 and SEQ ID NO:8, residues 1316-1485.

Table 4 EST:yu23d11 sequences compared to H-Robo1. yu23d11 refers to the fragment of DNA which was sequenced. The fragment was sequenced from both ends generating the following two sequences: H77734 and H77733. yu23d11 is an unspliced cDNA. Only bases 59-215 match the coding sequence of H-Robo1 (502-651). The remaining bases are intronic. No bases of H77733 match the coding sequence of H-Robo1.

```
LRDDFRQNPSDVMVAVGEPAVMECQPPRGHPEPTISWKKDGSPLDDKDER  H-Robo1
LRDDFRQKPSDVMVAVGEPAVMECQPPRGHPEPTISWKKDGSPLDDKDER  EST H77734
```

There is an error in the sequence, a T to G change which results in the amino acid N being replaced by K. The sequence is shown below and has been reversed for clarity:

```
TACTTCGGGATGACTTCAGACAAAAACCTTCGGATGTCATGGTTGCAGTA  H-Robo1
TACTTCGGGATGACTTCAGACAAAACCCTTCGGATGTCATGGTTGCAGTA  EST H77734
   L  R  D  D  F  R  Q  K  P  S  D  V  M  V  A  V
                        N
```

Table 5 EST:yq76e12 sequences compared to H-Robo1. yq76e12 refers to the fragment of DNA which was sequenced. The fragment was sequenced from both ends generating the following two sequences: H52936 and H52937 (the latter has been reversed for clarity). The sequences can be seen to overlap in the middle. A gap indicates a frameshift error. Note that errors only occur in one sequence at any one position.

```
GPLVSDMDTDAPEEEEDEADMEVAKMQTRRLLLRGLEQTPASSV  H-Robo1
GPLVSDMDTDAPEEEEDEADMEVAKMQT.RLLLRGLEQTPASSV  EST H52936

GDLESSVTGSMINGWGSASEEDNISSGRSSVSSSDGSFFTDADF  H-Robo1
GDLESSVTGSMINGWGSASEEDNISSGRSSVSSSDGSFFTDADF  EST H52936
```

```
AQAVAAA AEYAGLKVARRQMQDA AGR RHFH AS QC PRPT  H-Robo1
AQAVAAA AEYAGLKVARRQMQDA AGR RHFH AF QC PRPT  EST H52936
   ?AAT A?YAGLKVARRQMRDA AGR RHFH AS QC PRPT  EST H52937

SPVSTDSNMSAAVMQKTRPAKKLKHQPGHLRRETYTDDLPPPPV  H-Robo1
SPVFTDSNM                                      EST H52936
SPVSTDSNMSAAVMQKTRPAKKLKHQPGHLRRETYTDDLPPPPV  EST H52937

PPPAIKSPTAQSKTQLEVRPVVVPKLPSMDARTDK            H-Robo1
PPPAIKSPTAQSKTQLEVRPVVVPKLPSMDARTDK            EST H52937
```

The subject domains provide Robo domain specific activity or function, such as Robo-specific cell, especially neuron modulating or modulating inhibitory activity, Robo-ligand-binding or binding inhibitory activity. Robo-specific activity or function may be determined by convenient *in vitro,* cell-based, or *in vivo* assays: e.g. *in vitro* binding assays, cell culture assays, in animals (e.g. gene therapy, transgenics, etc.), etc. Binding assays encompass any assay where the molecular interaction of a Robo polypeptide with a binding target is evaluated. The binding target may be a natural intracellular binding target, a Robo regulating protein or other regulator that directly modulates Robo activity or its localization; or non-natural binding target such as a specific immune protein such as an antibody, or a Robo specific agent such as those identified in screening assays such as described below. Robo-binding specificity may be assayed by binding equilibrium constants (usually at least about 10^7 M^{-1}, preferably at least about 10^8 M^{-1}, more preferably at least about 10^9 M^{-1}), by the ability of the subject polypeptide to function as negative mutants in Robo-expressing cells, to elicit Robo specific antibody in a heterologous host (e.g a rodent or rabbit), etc.

The claimed Robo polypeptides are isolated or pure: an "isolated" polypeptide is unaccompanied by at least some of the material with which it is associated in its natural state, preferably constituting at least about 0.5%, and more preferably at least about 5% by weight of the total polypeptide in a given sample and a pure polypeptide constitutes at least about 90%, and preferably at least about 99% by weight of the total polypeptide in a given sample. A polypeptide, as used herein, is a polymer of amino acids, generally at least 6 residues, preferably at least about 10 residues, more preferably at least about 25 residues, most

preferably at least about 50 residues in length. The Robo polypeptides and polypeptide domains may be synthesized, produced by recombinant technology, or purified from mammalian, preferably human cells. A wide variety of molecular and biochemical methods are available for biochemical synthesis, molecular expression and purification of the subject compositions, see e.g. Molecular Cloning, A Laboratory Manual (Sambrook, *et al.* Cold Spring Harbor Laboratory), Current Protocols in Molecular Biology (Eds. Ausubel, *et al.*, Greene Publ. Assoc., Wiley-Interscience, NY) or that are otherwise known in the art.

The invention provides binding agents specific to the claimed Robo polypeptides, including natural intracellular binding targets, etc., methods of identifying and making such agents, and their use in diagnosis, therapy and pharmaceutical development. For example, specific binding agents are useful in a variety of diagnostic and therapeutic applications, especially where pathology, wound repair incompetency or prognosis is associated with improper or undesirable axon outgrowth, orientation or inhibition thereof. Novel Robo-specific binding agents include Robo-specific receptors, such as somatically recombined polypeptide receptors like specific antibodies or T-cell antigen receptors (see, e.g Harlow and Lane (1988) Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory), natural intracellular binding agents identified with assays such as one-, two- and three-hybrid screens, non-natural intracellular binding agents identified in screens of chemical libraries such as described below, etc. Agents of particular interest modulate Robo function.

In a particular embodiment, the subject polypeptides are used to generate Robo- or human Robo-specific antibodies. For example, the Robo- and human Robo-specific peptides described above are covalently coupled to keyhole limpet antigen (KLH) and the conjugate is emulsified in Freunds complete adjuvant. Laboratory rabbits are immunized according to conventional protocol and bled. The presence of Robo-specific antibodies is assayed by solid phase immunosorbant assays using immobilized Robo polypeptides of SEQ ID NO:2, 4, 6, 8, 10 or 12. Human Robo-specific antibodies are characterized as uncross-reactive with non-human Robo polypeptides (SEQ ID NOS:2, 4, 6 and 12).

Accordingly, the invention provides methods for modulating cell function comprising the step of modulating Robo activity, e.g. by contacting the cell with a Robo inhibitor, e.g. inhibitory Robo deletion mutants, Robo-specific antibodies, etc. (supra). The target cell may reside in culture or in situ, i.e. within the natural host. The inhibitor may be provided in any convenient way, including by (i) intracellular expression from a recombinant nucleic acid or

(ii) exogenous contacting of the cell. For many in situ applications, the compositions are added to a retained physiological fluid such as blood or synovial fluid. For CNS administration, a variety of techniques are available for promoting transfer of the therapeutic across the blood brain barrier including disruption by surgery or injection, drugs which transiently open adhesion contact between CNS vasculature endothelial cells, and compounds which facilitate translocation through such cells. Robo polypeptide inhibitors may also be amenable to direct injection or infusion, topical, intratracheal/nasal administration e.g. through aerosol, intraocularly, or within/on implants e.g. fibers e.g. collagen, osmotic pumps, grafts comprising appropriately transformed cells, etc. A particular method of administration involves coating, embedding or derivatizing fibers, such as collagen fibers, protein polymers, etc. with therapeutic proteins. Other useful approaches are described in Otto et al. (1989) J Neuroscience Research 22, 83-91 and Otto and Unsicker (1990) J Neuroscience 10, 1912-1921. Generally, the amount administered will be empirically determined, typically in the range of about 10 to 1000 μg/kg of the recipient and the concentration will generally be in the range of about 50 to 500 μg/ml in the dose administered. Other additives may be included, such as stabilizers, bactericides, etc. will be present in conventional amounts. For diagnostic uses, the inhibitors or other Robo binding agents are frequently labeled, such as with fluorescent, radioactive, chemiluminescent, or other easily detectable molecules, either conjugated directly to the binding agent or conjugated to a probe specific for the binding agent.

The amino acid sequences of the disclosed Robo polypeptides are used to back-translate Robo polypeptide-encoding nucleic acids optimized for selected expression systems (Holler et al. (1993) Gene 136, 323-328; Martin et al. (1995) Gene 154, 150-166) or used to generate degenerate oligonucleotide primers and probes for use in the isolation of natural Robo-encoding nucleic acid sequences ("GCG" software, Genetics Computer Group, Inc, Madison WI). Robo-encoding nucleic acids used in Robo-expression vectors and incorporated into recombinant host cells, e.g. for expression and screening, transgenic animals, e.g. for functional studies such as the efficacy of candidate drugs for disease associated with Robo-modulated cell function, etc.

The invention also provides nucleic acid hybridization probes (Tables 6, 7) and replication / amplification primers (Tables 7, 8) having a Robo cDNA specific sequence comprising SEQ ID NO:1, 3, 5, 7, 9 or 11 and sufficient to effect specific hybridization

thereto (i.e. specifically hybridize with SEQ ID NO:1, 3, 5, 7, 9 or 11, respectively, in the presence of CDO cDNA.

Table 5. Hybridisation Probes for Human Roundabout 1

Immunoglobulin Domain #1

CCACCTCGCATTGTTGAACACCCTTCAGACCTGATTGTCTCAAAAGGAGAACCTGCAACTTTGAACTGCAAAGCT
GAAGGCCGCCCCACACCCACTATTGAATGGTACAAAGGGGGAGAGAGAGTGGAGACAGACAAAGATGACCCTCGC
TCACACCGAATGTTGCTGCCGAGTGGATCTTTATTTTTCTTACGTATAGTACATGGACGGAAAAGTAGACCTGAT
GAAGGAGTCTATGTCTGTGTAGCAAGGAATTACCTTGGAGAGGCTGTGAGCCACAATGCATCGCTGGAAGTAGCC
ATA

Immunoglobulin Domain#2

CTTCGGGATGACTTCAGACAAAACCCTTCGGATGTCATGGTTGCAGTAGGAGAGCCTGCAGTAATGGAATGCCAA
CCTCCACGAGGCCATCCTGAGCCCACCATTTCATGGAAGAAAGATGGCTCTCCACTGGATGATAAAGATGAAAGA
ATAACTATACGAGGAGGAAAGCTCATGATCACTTACACCCGTAAAAGTGACGCTGGCAAATATGTTTGTGTTGGT
ACCAATATGGTTGGGGAACGTGAGAGTGAAGTAGCCGAGCTGACTGTCTT

Immunoglobulin Domain #3

AGAGAGACCATCATTTGTGAAGAGACCCAGTAACTTGGCAGTAACTGTGGATGACAGTGCAGAATTTAAATGTGA
GGCCCGAGGTGACCCTGTACCTACAGTACGATGGAGGAAAGATGATGGAGAGCTGCCCAAATCCAGATATGAAAT
CCGAGATGATCATACCTTGAAAATTAGGAAGGTGACAGCTGGTGACATGGGTTCATACACTTGTGTTGCAGAAAA
TATGGTGGGCAAAGCTGAAGCATCTGCTACTCTGACTGTTCAAGAACC

Immunoglobulin Domain #4

CCACATTTTGTTGTGAAACCCCGTGACCAGGTTGTTGCTTTGGGACGGACTGTAACTTTTCAGTGTGAAGCAACC
GGAAATCCTCAACCAGCTATTTTCTGGAGGAGAGAAGGGAGTCAGAATCTACTTTTCTCATATCAACCACCACAG
TCATCCAGCCGATTTTCAGTCTCCCAGACTGGCGACCTCACAATTACTAATGTCCAGCGATCTGATGTTGGTTAT
TACATCTGCCAGACTTTAAATGTTGCTGGAAGCATCATCACAAAGGCATATTTGGAAGTTACAGATGTGATTGCA

Immunoglobulin Domain #5

GATCGGCCTCCCCCAGTTATTCGACAAGGTCCTGTGAATCAGACTGTAGCCGTGGATGGCACTTTCGTCCTCAGC
TGTGTGGCCACAGGCAGTCCAGTGCCCACCATTCTGTGGAGAAAGGATGGAGTCCTCGTTTCAACCCAAGACTCT
CGAATCAAACAGTTGGAGAATGGAGTACTGCAGATCCGATATGCTAAGCTGGGTGATACTGGTCGGTACACCTGC
ATTGCATCAACCCCCAGTGGTGAAGCAACATGGAGTGCTTACATTGAAGTTCAAGAATTTG

Fibronectin Domain #1

GAGTTCCAGTTCAGCCTCCAAGACCTACTGACCCAAATTTAATCCCTAGTGCCCCATCAAAACCTGAAGTGACAG
ATGTCAGCAGAAATACAGTCACATTATCGTGGCAACCAAATTTGAATTCAGGAGCAACTCCAACATCTTATATTA
TAGAAGCCTTCAGCCATGCATCTGGTAGCAGCTGGCAGACCGTAGCAGAGAATGTGAAAACAGAAACATCTGCCA
TTAAAGGACTCAAACCTAATGCAATTTACCTTTTCCTTGTGAGGGCAGCTAATGCATATGGAATTAGTGATC

Fibronectin Domain #2

CAAGCCAAATATCAGATCCAGTGAAAACACAAGATGTCCTACCAACAAGTCAGGGGGTGGACCACAAGCAGGTCC
AGAGAGAGCTGGGAAATGCTGTTCTGCACCTCCACAACCCCACCGTCCTTTCTTCCTCTTCCATCGAAGTGCACT
GGACAGTAGATCAACAGTCTCAGTATATACAAGGATATAAAATTCTCTATCGGCCATCTGGAGCCAACCACGGAG
AATCAGACTGGTTAGTTTTTGAAGTGAGGACGCCAGCCAAAAACAGTGTGGTAATCCCTGATCTCAGAAAGGGAG
TCAACTATGAAATTAAGGCTCGCCCTTTTTTTAATGAATTTCAAGGAGCAG

Fibronectin Domain #3

ATAGTGAAATCAAGTTTGCCAAAACCCTGGAAGAAGCACCCAGTGCCCCACCCCAAGGTGTAACTGTATCCAAGA
ATGATGGAAACGGAACTGCAATTCTAGTTAGTTGGCAGCCACCTCCAGAAGACACTCAAAATGGAATGGTCCAAG
AGTATAAGGTTTGGTGTCTGGGCAATGAAACTCGATACCACATCAACAAAACAGTGGATGGTTCCACCTTTTCCG
TGGTCATTCCCTTTCTTGTTCCTGGAATCCGATACAGTGTGGAAGTGGCAGCCAGCACTGGGGCTGGGTCTGGGG
TAAAG

Transmembrane Domain

AGATTTCAGATGTGGTGAAGCAGCCGGCCTTCATAGCAGGTATTGGAGCAGCCTGTTGGATCATCCTCATGGTCT
TCAGCATCTGGCTTTATCGACACCG

Cytoplasmic Motif #1

AATCTGAAGGATGGGCGTTTTGTCAATCCATCAGGGCAGCCTACTCCTTACGCCACCACTCAGCTCATCCAGTCA
AACCTCAGCAACAACATGAACAATG

Cytoplasmic Motif #2

CCCAAGGTACCAAAACAGGGTGGCATGAACTGGGCAGACCTGCTTCCTCCTCCCCCAGCACATCCTCCTCCACAC
AGCAATAGCGAAGAGTACAACATTT

Cytoplasmic Motif #3

CCAGCCAGGACATCTGCGCAGAGAAACCTACACAGATGATCTTCCACCACCTCCTGTGCCGCCACCTGCTATAAA
GTCACCTACTGCCCAATCCAAGACA

Table 6. Hybridisation Probes for Human Roundabout 2

Immunoglobulin Domain #4

CAGATTGTTGCTCAAGGTCGAACAGTGACATTTCCCTGTGAAACTAAAGGAAACCCACAGCCAGCTGTTTTTTGG

CAGAAAGAAGGCAGCCAGAACCTACTTTTCCCAAACCAACCCCAGCAGCCCAACAGTAGATGCTCAGTGTCACCA

ACTGGAGACCTCACAATCACCAACATTCAACGTTCCGACGCGGGTTACTACATCTGCCAGGCTTTAACTGTGGCA

GGAAGCATTTTAGCAAAAGCTCAACTGGAGGTTACTGATGTTTTGACA

Immunoglobulin Domain #5

GATAGACCTCCACCTATAATTCTACAAGGCCCAGCCAACCAAACGCTGGCAGTGGATGGTACAGCGTTACTGAAA

TGTAAAGCCACTGGTGATCCTCTTCCTGTAATTAGCTGGTTAAAGGAGGGATTTACTTTTCCGGGTAGAGATCCA

AGAGCAACAATTCAAGAGCAAGGCACACTGCAGATTAAGAATTTACGGATTTCTGATACTGGCACTTATACTTGT

GTGGCTACAAGTTCAAGTGGAGAGGCTTCCTGGAGTGCAGTGCTGGATGTGACAGAGTCT

Fibronectin Domain #1

GGAGCAACAATCAGTAAAAACTATGATTTAAGTGACCTGCCAGGGCCACCATCCAAACCGCAAGTCACTGATGTT

ACTAAGAACAGTGTCACCTTGTCCTGGCAGCCAGGTACCCCTGGAACCCTTCCAGCAAGTGCATATATCATTGAG

GCTTTCAGCCAATCAGTGAGCAACAGCTGGCAGACCGTGGCAAACCATGTAAAGACCACCCTCTATACTGTAAGA

GGACTGCGGCCCAATACAATCTACTTATTCATGGTCAGAGCGATCAACCCCAAGGTYTCAGTGACCCAAGT

Table 7. Primer Pairs for PCR of Human Roundabout 1 Domains

Immunoglobulin Domain #1

Forward: 5' CCACCTCGCATTGTTGAACACCCTTCAGAC 3'

Reverse: 5' ATGGCTACTTCCAGCGATGCATTGTGGCTC 3'

Immunoglobulin Domain #2

Forward: 5' CTTCGGGATGACTTCAGACAAAACCCTTCG 3'

Reverse: 5' TAAGACAGTCAGCTCGGCTACTTCACTCTC 3'

Immunoglobulin Domain #3

Forward: 5' AGAGAGACCATCATTTGTGAAGAGACCCAG 3'

Reverse: 5' AGGTTCTTGAACAGTCAGAGTAGCAGATGC 3'

Immunoglobulin Domain #4

Forward: 5' CCACATTTTGTTGTGAAACCCCGTGACCAG 3'

Reverse: 5' TGCAATCACATCTGTAACTTCCAAATATGC 3'

Immunoglobulin Domain #5

Forward: 5' ATCGGCCTCCCCCAGTTATTCGACAAGGTC 3'

Reverse: 5' CAAATTCTTGAACTTCAATGTAAGCACTCC 3'

Fibronectin Domain #1

Forward: 5' GAGTTCCAGTTCAGCCTCCAAGACCTACTG 3'

Reverse: 5' TCACTAATTCCATATGCATTAGCTGCCCTC 3'

Fibronectin Domain #2

Forward: 5' CAAGCCAAATATCAGATCCAGTGAAAACAC 3'

Reverse: 5' ATCTGCTCCTTGAAATTCATTAAAAAAAGG 3'

Fibronectin Domain #3

Forward: 5' ATAGTGAAATCAAGTTTGCCAAAACCCTG 3'

Reverse: 5' CTCTTTACCCCAGACCCAGCCCCAGTGCTG 3'

Transmembrane Domain

Forward: 5' GGACCAAGTCAGCCTCGCTCAGCAGATTTC 3'

Reverse: 5' ACTAGTAAGTCCGTTTCTCTTCTTGCGGTG 3'

Cytoplasmic Motif #1

Forward: 5' CTGAAGGATGGGCGTTTTGTCAATCCATC 3'

Reverse: 5' GTCCCAGTGGTTTCCAGTGCTTCTCGCCAG 3'

Cytoplasmic Motif #2

Forward: 5' GGCACAAGAAAGGGGCAAGAACACCCAAGG 3'

Reverse: 5' ATAGCTTTCATCTACAGAAATGTTGTACTC 3'

Cytoplasmic Motif #3

Forward: 5' ACCAGACCAGCCAAGAAACTGAAACACCAG 3'

Reverse: 5' GTACTTCCAGCTGTGTCTTGGATTGGGCAG 3'

Table 8. Human Roundabout 2 Primer Pairs

Immunoglobulin Domain #4

Forward: 5' GTTGCTCAAGGTCGAACAGTGACATTTCCC 3'

Reverse: 5' TGTCAAAACATCAGTAACCTCCAGTTGAGC 3'

Immunoglobulin Domain #5

Forward: 5' GATAGACCTCCACCTATAATTCTACAAGGC 3'

Reverse: 5' GACTCTGTCACATCCAGCACTGCACTCCAG 3'

Fibronectin Domain #1

Forward: 5' CAATCAGTAAAAACTATGATTTAAGTG 3'

Reverse: 5' TCGCTCTGACCATGAATAAGTAGATTG 3'

Such primers or probes are at least 12, preferably at least 24, more preferably at least 36 and most preferably at least 96 bases in length. Demonstrating specific hybridization generally requires stringent conditions, for example, hybridizing in a buffer comprising 30% formamide in 5 x SSPE (0.18 M NaCl, 0.01 M $NaPO_4$, pH7.7, 0.001 M EDTA) buffer at a temperature of 42°C and remaining bound when subject to washing at 42°C with 0.2 x SSPE; preferably hybridizing in a buffer comprising 50% formamide in 5 x SSPE buffer at a temperature of 42°C and remaining bound when subject to washing at 42°C with 0.2 x SSPE buffer at 42°C. Robo nucleic acids can also be distinguished using alignment algorithms, such as BLASTX (Altschul *et al.* (1990) Basic Local Alignment Search Tool, J Mol Biol 215, 403-410).

The subject nucleic acids are of synthetic/non-natural sequences and/or are isolated, i.e. unaccompanied by at least some of the material with which it is associated in its natural state, preferably constituting at least about 0.5%, preferably at least about 5% by weight of total nucleic acid present in a given fraction, and usually recombinant, meaning they comprise a non-natural sequence or a natural sequence joined to nucleotide(s) other than that which it is joined to on a natural chromosome. The subject recombinant nucleic acids comprising the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9 or 11, or fragments thereof, contain such sequence or fragment at a terminus, immediately flanked by (i.e. contiguous with) a sequence other than that which it is joined to on a natural chromosome, or flanked by a native flanking region fewer than 10 kb, preferably fewer than 2 kb, more preferably fewer than 500 bp, which is at a terminus or is immediately flanked by a sequence other than that which it is joined to on a natural chromosome. While the nucleic acids are usually RNA or DNA, it is

often advantageous to use nucleic acids comprising other bases or nucleotide analogs to provide modified stability, etc.

In a particular embodiment, expressed sequence tags EST;yu23d11, Accession #H77734 and EST;yq76e12, Accession #H52936, and deletion mutants thereof, are not within the scope of the present invention. In another embodiment, the subject Robo nucleic acids exclude the corresponding regions of the disclosed natural human Robo I nucleic acids, i.e. SEQ ID NO:7, nucleotides 500-651 and SEQ ID NO:7, nucleotides 3945-4455.

Table 10. Exemplary differences between H52936 and corresponding human Robo I sequences.

(1) At position 86, there is a T instead of an A. The new codon therefore reads TGA (Stop) instead of AGA (R).

(2) There is a missing G at position 286-7, causing a frameshift.

(3) There is an extra G at position 334, causing a frameshift.

(4) There is an extra T at position 344, causing a frameshift.

(5) There is an extra N at position 357, causing a frameshift.

(6) There is a T instead of a C at 362. The new codon reads TTT (F) instead of TCT (S).

(7) There is an extra T at position 364, causing a frameshift.

(8) There is an extra N at position 370, causing a frameshift and a changed amino acid (the codon TTN is ambiguous).

(9) There are two Ts at position 394 and 395 instead of a C, causing a frameshift and amino acid changes.

Table 11 . Exemplary differences between H52937 (reverse sequence) and corresponding human Robo I sequences.

(1) There are multiple errors in the first 30 bases.

(2) At position 63, a G replaces an A. The new codon CGG codes for R instead of CAG for Q.

(3) The EST ends by joining to part of the human glycophorin B gene (353-442)

The subject nucleic acids find a wide variety of applications including use as translatable transcripts, hybridization probes, PCR primers, diagnostic nucleic acids, etc.; use in detecting the presence of Robo genes and gene transcripts and in detecting or amplifying

nucleic acids encoding additional Robo homologs and structural analogs. In diagnosis, Robo hybridization probes find use in identifying wild-type and mutant Robo alleles in clinical and laboratory samples. Mutant alleles are used to generate allele-specific oligonucleotide (ASO) probes for high-throughput clinical diagnoses. In therapy, therapeutic Robo nucleic acids are used to modulate cellular expression or intracellular concentration or availability of active Robo.

The invention provides efficient methods of identifying agents, compounds or lead compounds for agents active at the level of a Robo modulatable cellular function. Generally, these screening methods involve assaying for compounds which modulate Robo interaction with a natural Robo binding target. A wide variety of assays for binding agents are provided including labeled *in vitro* protein-protein binding assays, immunoassays, cell based assays, etc. The methods are amenable to automated, cost-effective high throughput screening of chemical libraries for lead compounds. Identified reagents find use in the pharmaceutical industries for animal and human trials; for example, the reagents may be derivatized and rescreened in *in vitro* and *in vivo* assays to optimize activity and minimize toxicity for pharmaceutical development.

Cell and animal based neural guidance/repulsion assays are described in detail in the experimental section below. *In vitro* binding assays employ a mixture of components including a Robo polypeptide, which may be part of a fusion product with another peptide or polypeptide, e.g. a tag for detection or anchoring, etc. The assay mixtures comprise a natural intracellular Robo binding target. While native full-length binding targets may be used, it is frequently preferred to use portions (e.g. peptides) thereof so long as the portion provides binding affinity and avidity to the subject Robo polypeptide conveniently measurable in the assay. The assay mixture also comprises a candidate pharmacological agent. Candidate agents encompass numerous chemical classes, though typically they are organic compounds; preferably small organic compounds and are obtained from a wide variety of sources including libraries of synthetic or natural compounds. A variety of other reagents may also be included in the mixture. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, protease inhibitors, nuclease inhibitors, antimicrobial agents, etc. may be used.

The resultant mixture is incubated under conditions whereby, but for the presence of the candidate pharmacological agent, the Robo polypeptide specifically binds the cellular

binding target, portion or analog with a reference binding affinity. The mixture components can be added in any order that provides for the requisite bindings and incubations may be performed at any temperature which facilitates optimal binding. Incubation periods are likewise selected for optimal binding but also minimized to facilitate rapid, high-throughput screening.

After incubation, the agent-biased binding between the Robo polypeptide and one or more binding targets is detected by any convenient way. Where at least one of the Robo or binding target polypeptide comprises a label, the label may provide for direct detection as radioactivity, luminescence, optical or electron density, etc. or indirect detection such as an epitope tag, etc. A variety of methods may be used to detect the label depending on the nature of the label and other assay components, e.g. through optical or electron density, radiative emissions, nonradiative energy transfers, etc. or indirectly detected with antibody conjugates, etc.

A difference in the binding affinity of the Robo polypeptide to the target in the absence of the agent as compared with the binding affinity in the presence of the agent indicates that the agent modulates the binding of the Robo polypeptide to the Robo binding target. For example, in the cell-based assay also described below, a difference in Robo-dependent modulation of axon outgrowth or orientation in the presence and absence of an agent indicates the agent modulates Robo function. A difference, as used herein, is statistically significant and preferably represents at least a 50%, more preferably at least a 90% difference.

The following experimental section and examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

Cloning of the *roundabout* Gene. The *robo*^{1} allele was mapped to the *plexus-brown* interval on the right arm of the second chromosome by recombination mapping; the numbers of recombinants suggested a map position very close to *plexus* at 58F/59A. One deficiency [*Df(2R)P*, which deletes 58E3/F1 through 60D14/E2] fails to complement *robo* mutations, two other deficiencies [*Df(2R)59AB* and *Df(2R)59AD,* which delete 59A1/3 through 59B1/2 and 59A1/3 through 59D1/4 respectively] do complement *robo*, and a duplication [*Dp(2;Y)bw*$^{+}$*Y*, which duplicates 58F1/59A2 through 60E3/F1] rescues *robo* mutations. This mapping places *robo* in the 58F/59A region.

We initiated chromosomal walks from P1 clones mapped to the region, beginning from the distal side using clone DS02204 and from the proximal side using clone DS05609. We used cosmid clones (Tamkun et al., 1992) to complete a walk of ~150 kb. We then looked for RFLPs in the recombinants between the multiple marked chromosome and the *robo* mutant chromosome. A 6.8kb EcoRI fragment from cosmid 106-5 identified a HindII RFLP on the mapping chromosome that was present on a single *robo* mutant recombinant line. This fragment identified a proximal limit for the location of *robo*. Further deficiencies in this region were then tested (Kerrebrock et al., 1995). Of these deficiencies, *Df(2R)X58-5* and *Df(2R)X58-12* remove *robo* while *Df(2R)X58-1* does not. *Df(2R)X58-12* fails to complement *Df(2R)59AB* yet complements *Df(2R)59AD* indicating that *Df(2R)59AB* extends further proximal; this proximal endpoint provides a distal limit for the location of *robo*. Probes from the walk were used to identify the breakpoints of these deficiencies (Figure 1A). *Df(2R)X58-1* breaks in a 9.6 kb EcoRI/BamHI fragment within cosmid GJ12, whereas *Df(2R) 59AB* breaks in a 8 kb BamHI/EcoRI fragment within cosmid 106-1435. This reduces the location of *robo* to a 75 kb region bounded by these restriction fragments. Hybridization of 0-16 hr poly-A^+ embryonic Northern blots with cosmids GJ12, 106-12, and 106-1435 revealed at least five transcripts. Reverse Northern mapping identified the regions containing these transcripts (Figure 1A). These regions were used as probes to isolate cDNAs. Seven different cDNAs were isolated and analyzed by in situ hybridization. The expression pattern of five of these transcripts allowed us to tentatively discount them as encoding for *robo* since they were not expressed in the embryonic CNS at the appropriate stage. Of the two cDNAs remaining, 12-1 appeared by its size and expression the most likely candidate for *robo*. A 16 kb XbaI fragment including the 12-1 transcript and a region 5' to the transcript is capable of rescuing the *robo* mutant.

roundabout Encodes a Member of the Immunoglobulin Superfamily. We recovered and sequenced overlapping cDNA clones corresponding to the 12-1 transcription unit. A single long open reading frame (ORF) that encodes 1395 amino acids was identified (D1 in Table 1). Conceptual translation of the ORF reveals the Robo protein to be a member of the Ig superfamily; Robo's ectodomain contains five immunoglobulin (Ig)-like repeats followed by three fibronectin (Fn) type-III repeats. The predicted ORF also contains a transmembrane domain and a large 457 amino acid (a.a.) cytoplasmic domain. Hydropathy analysis of the Robo sequence indicates a single membrane spanning domain of 25 a.a. (Kyte and Doolittle,

1982) plus a signal sequence with a predicted cleavage site between G51 and Q52 (Nielsen et al 1997).

We identify the 12-1 transcript as encoding *robo* based on several criteria. First, the embryonic *robo* phenotype can be rescued by the 16 kb XbaI genomic fragment containing this cDNA; no other transcripts are contained in this 16 kb XbaI fragment. Second, we identified a CfoI RFLP associated with the allele *robo*^{6}. This polymorphism is due to a change of nucleotide 332 of the ORF from G to A, which results in a change of Gly_{111} to Asp. Gly111 is in the first Ig domain (Figure 2), and is conserved in all Robo homologues identified. The change is specific to the allele *robo*^{6} and is not seen in the parental chromosome or in any of the other seven alleles, all of which were generated from the same parental genotype. Third, the production of antibodies (below) which recognize the Robo protein reveals that the alleles *robo*^{1}, *robo*^{2}, *robo*^{3}, *robo*^{4} and *robo*^{5} do not produce Robo protein (Table 12).

Table 12. *robo* Mutant Alleles

Allele	Synonym	Class
robo^1	GA285	Protein null
robo^2	GA1112	Protein null
robo^3	Z14	Protein null
robo^4	Z570	Protein null
robo^5	Z1772	Protein null
robo^6	Z1757	Protein positive; Gly_{111} to Asp
robo^7	Z2130	Reduced protein levels
robo^8	Z3127	Protein positive

All alleles were generated by EMS mutagenesis of *FasIII* null chromosomes. Each of these alleles appear to represent a complete, or near complete, loss-of-function phenotype for *robo,* since the mutant phenotype observed when these alleles are placed over a chromosome deficient for the *robo* locus [Df(2R) X58-5] is indistinguishable from the homozygous allele.

Finally, transgenic neural expression of *robo* rescues the midline crossing phenotype of *robo* mutants (see below).

Developmental Northern blot analysis using both cDNA and genomic probes suggests that *robo* is encoded by a single transcript of ~7500 bp. We sequenced genomic DNA and identified 17 introns within the sequence of which 14 are only 50-75 bp in length plus three

introns of 843 bp, 236 bp, and 110 bp (Figure 1B). The precise start point of the transcript has not been determined.

A Family of Evolutionarily Conserved Robo-like Proteins. The presence of five Ig and three Fn domains, a transmembrane domain, and a long (452 a.a.) cytoplasmic region indicates that Robo may be a receptor and signaling molecule. The netrin receptor DCC/Frazzled/UNC-40 has a related domain structure, with 6 Ig and 4 Fn domains and a similarly long cytoplasmic region (Keino-Masu et al., 1996; Chan et al., 1996; Kolodziej et al., 1996). The only currently known protein with a "5 + 3" organization is CDO (Kang et al., 1997). However, CDO is only distantly related to Robo (15-33% a.a. identity between corresponding Ig and FN domains).

We identified other "5 + 3" proteins in vertebrates whose amino acid identity exceeds that of CDO and represent Robo homologues. A human expressed sequence tag (EST; yu23d11, Accession #H77734) shows high homology to the second Ig domain of *robo* and was used to probe a human fetal brain cDNA library (Stratagene). The clones recovered correspond to a human gene with five Ig and three Fn domains (Figure 2). Exemplary functional Robo domains are listed in Tables 13-17 (the corresponding encoding nucleic acids are readily discernable from the corresponding nucleic acid sequences of Sequence Listing).

Table 13. Exemplary domains of human Robo 1, by amino acid sequence positions

Signal sequence:	6-21
First Immunoglobulin domain:	68-167
Second Immunoglobulin domain:	168-258
Third Immunoglobulin domain:	259-350
Fourth Immunoglobulin domain:	351-450
Fifth Immunoglobulin domain:	451-546
First Fibronectin domain:	547-644
Second Fibronectin domain:	645-761
Third Fibronectin domain:	762-862
Transmembrane domain:	896-917
Cytoplasmic motif #1:	1070-1079
Cytoplasmic motif #2:	1181-1195
Cytoplasmic motif #3:	1481-1488

Table 14. Exemplary domains of human Robo II, by amino acid sequence positions

Fourth Immunoglobulin domain:	1-91
Fifth Immunoglobulin domain:	92-185
First Fibronectin domain:	186-282

Table 15. Exemplary domains of drosophila Robo 1, by amino acid sequence positions

Signal sequence:	30-46
First Immunoglobulin domain:	56-152
Second Immunoglobulin domain:	153-251
Third Immunoglobulin domain:	252-344
Fourth Immunoglobulin domain:	345-440
Fifth Immunoglobulin domain:	441-535
First Fibronectin domain:	536-635
Second Fibronectin domain:	636-753
Third Fibronectin domain:	754-854
Transmembrane domain:	915-938
Cytoplasmic motif #1:	1037-1046
Cytoplasmic motif #2:	1098-1119
Cytoplasmic motif #3:	1262-1269

Table 16. Exemplary domains of drosophila Robo II, by amino acid sequence positions

Immunoglobulin domain #1:	4-99
Immunoglobulin domain #2:	100-192
Immunoglobulin domain #3:	193-296
Immunoglobulin domain #4:	297-396
Immunoglobulin domain #5:	397-494
Fibronectin domain #1:	495-595
Fibronectin domain #2:	596-770
Fibronectin domain #3:	771-877
Transmembrane domain:	906-929
Conserved cytoplasmic motif #1:	1075-1084

Table 17. Exemplary domains of C. elegans Robo 1, by amino acid sequence positions

First Immunoglobulin domain:	30-129
Second Immunoglobulin domain:	130-223
Third Immunoglobulin domain:	224-315
Fourth Immunoglobulin domain:	316-453
Fifth Immunoglobulin domain:	454-543
First Fibronectin domain:	544-643
Second Fibronectin domain:	644-766
Third Fibronectin domain:	767-865
Transmembrane domain:	900-922
Cytoplasmic motif #1:	1036-1045
Cytoplasmic motif #2:	1153-1163
Cytoplasmic motif #3:	1065-1074

The homology is particularly high in the first two Ig domains (58% and 48% a.a. identity respectively, compared to 26% and 30% for the same two Ig domains between D-Robo1 and CDO) and together with the overall identity throughout the extracellular region and the presence of three conserved cytoplasmic motifs has led us to designate this as the human *roundabout 1* gene (*H-robo1*). Database searching reveals a nucleotide sequence corresponding to *H-robo1* in the database, *DUTT1*, which differs in the signal sequence suggesting alternative splicing, a 9 bp insertion and seven single base pair changes. Five ESTs (see Experimental Procedures) show high sequence similarity to the cytoplasmic domain of *H-robo1*. Sequencing of cDNAs isolated using one of these ESTs as a probe confirmed a second human *roundabout* gene (*H-robo2*).

Degenerate PCR primers based on conserved sequences between *H-robo1* and *D-robo1* were used to isolate a PCR fragment from a rat embryonic E13 brain cDNA library. The fragment was used to probe an E13 spinal cord cDNA library, resulting in the isolation of a full length Rat *robo* gene (*R-robo1*). The predicted protein shows high sequence identitiy (>95%) with *H-robo1* over the entire length. The 5' sequences of different *R-robo1* cDNA clones indicates that this gene is alternatively spliced in a similar fashion to *H-robo1/DUTTI*. We used a similar approach to isolate cDNA clones for *R-robo2*, which is highly homologous to *H-robo2*.

The mouse EST vi92e02 is highly homologous to the cytoplasmic portion of *H-robo1*. The *C. elegans Sax-3* gene is also a *robo* homologue (Table 1; Zallen et al., 1997). A second Drosophila *robo* gene (*D-robo2*) is also predicted from analysis of genomic sequence in the public database. Taken together these data indicate that Robo is the founding member of a new subfamily of Ig superfamily proteins with at least one member in nematode, two in Drosophila, two in rat, and two in human.

The alignment of the Robo family proteins reveals that the first and second Ig domains are the most highly conserved portion of the extracellular domain. The cytoplasmic domains are highly divergent except for the presence of three highly conserved motifs (Table 18).

Table 18. Conserved Cytoplasmic Motifs: Amino acid alignments of the three conserved cytoplasmic motifs are shown below the structure; in C.elegans *robo*, motifs #2 and #3 have been switched to provide a better alignment.

Conserved Cytoplasmic Motif #1

```
PDNPTPYATTMIIGTSS  1050 Drosophila roundabout-I
SGQPTPYATTQLIQSNL  1083 Human roundabout-I
NASPAPYATSSILSPHQ  1088 Drosophila roundabout-II
HDDPSPYATTTLVLSNQ  1049 C.elegans roundabout
   PtPYATT.hh....       Consensus (where h is I, L or V)
```

Conserved Cytoplasmic Motif #2

```
INWSE.FLPPPPEHPPPSSTYG.Y  1119 Drosophila roundabout-I
MNWAD.LLPPPPAHPPPHSNSEEY  1202 Human roundabout-I
STWANVPLPPPPVQPLPGTELEHY    31 Human roundabout-II
KTLMD.FIPPPPSNPPPP.GGHVY  1168 C.elegans roundabout-I
 nW...hhPPPP. PPP.s....Y Consensus (where h is hydrophobic)
```

Conserved Cytoplasmic Motif #3

```
PSPMQPPPPVPVPEGW.Y  1273 Drosophila roundabout-I
YTDDLPPPPVPPPAIKSP  1493 Human roundabout-I
YADDLPPPPVPPPAIKSP    90 Mouse roundabout-I
```

```
RAPAMPTNPVPPEPPARY  1077 C.elegans roundabout
.....PPPPVPPP....          Consensus
```

The consensus for the first motif is PtPYATTxhh, where x is any amino acid and h is I, L, or V. The presence of a tyrosine in the center of the motif indicates a site for phosphorylation. The other two motifs consist of runs of prolines separated by one or two amino acids and are reminiscent of binding sites for SH3 domains. In particular, the LPPP sequence in motif #2 provides a good binding site for the Drosophila Enabled protein or its mammalian homologue Mena (Niebuhr et al., 1997). All three of these conserved sites can function as binding sites for domains (e.g. SH3 domains) of linker/adapter proteins functioning in Robo-mediated signal transduction.

Robo is Regionally Expressed on Longitudinal Axons in the Drosophila Embryo. In order to determine the role that *robo* might play in regulating axon crossing behavior, we examined the *robo* expression pattern in the embryonic CNS. The in situ hybridization pattern of *robo* mRNA in Drosophila shows it to have elevated and widespread expression in the CNS. We raised a monoclonal antibody (MAb 13C9) against part of the extracellular portion (amino acids 404-725) of the protein to visualize Robo expression. Robo is first seen in the embryo weakly expressed in lateral stripes during germband extension. At the onset of germband retraction, Robo expression is observed in the neuroectoderm. By the end of stage 12, as the growth cones first extend, Robo is seen on growth cones which project ipsilaterally, including pCC, aCC, MP1, dMP2, and vMP2. Strikingly, little or no Robo expression is observed on commissural growth cones as they extend towards and across the midline. However, as these growth cones turn to project longitudinally, their level of Robo expression dramatically increases. Robo is expressed at high levels on all longitudinally-projecting growth cones and axons. In contrast, Robo is expressed at nearly undetectable levels on commissural axons. This is striking since ~90% of axons in the longitudinal tracts also have axon segments crossing in one of the commissures. Thus, Robo expression is regionally restricted. Robo expression is also seen at a low level throughout the epidermis and at a higher level at muscle attachment sites. In stage 16-17 embryos, faint Robo staining can be seen in the commissures but at levels much lower than observed in the longitudinal tracts.

Immunoelectron Microscopy of Robo. We used immunoelectron microscopy to examine Robo localization at higher resolution. In stage 13 embryos, Robo is expressed at

higher levels on growth cones and filopodia in the longitudinal tracts than on the longitudinal axons themselves. This localization is consistent with the model that Robo functions as a guidance receptor. The increased sensitivity of immunoelectron microscopy reveals the presence of very low levels of Robo protein on the surface of commissural axons. In addition, Robo-positive vesicles can be seen inside the commissural axons, possibly representing transport of Robo to the growth cone. Finally, by reconstructing the path of single axons by use of serial sections, we confirm that Robo expression is greatly up-regulated after individual axons turn from the commissure into a longitudinal tract. The expression of Robo on non-crossing and post-crossing axons and its higher level of expression on growth cones and its filopodia, provide a model where Robo functions as an axon guidance receptor for a repulsive midline cue.

Transgenic Expression of Robo. We hypothesized that if Robo is indeed a growth cone receptor for a midline repellent, then pan-neural expression of Robo protein during the early stages of axon outgrowth might lead to a *robo* gain-of-function phenotype similar to the *comm* loss-of-function and opposite of the *robo* loss-of-function. To test this hypothesis, we cloned a *robo* cDNA containing the complete ORF but lacking most of its untranslated regions (UTRs) downstream of the UAS promoter in the pUAST vector and generated transgenic flies for use in the GAL4 system (Brand and Perrimon, 1993). Expression of *robo* in all neurons was achieved by crossing the *UAS-robo* flies to either the *elav-GAL4* or *scabrous-GAL4* lines.

Surprisingly, pan-neural expression of *robo* mRNA did not produce a strong axon scaffold phenotype as assayed with MAb BP102. Staining with anti-Fas II (MAb 1D4) revealed subtle fasciculation defects, but overall the axon scaffold looked quite normal. An insight into why we failed to observe a stronger *robo* ectopic expression phenotype was provided by staining these embryos with the anti-Robo MAb. Interestingly, the Robo protein, although expressed at higher levels than in wild type, remains restricted as in wild type, i.e., high levels of expression on the longitudinal portions of axons and very low levels on the commissures. This result indicates that there must be strong regulation of Robo expression, probably post-translational, that assures its localization to longitudinal axon segments. Such a mechanism could operate by the regulation of protein translation, transport, insertion, internalization and/or stability.

We used these transgenic flies to rescue *robo* mutants. Expression of *robo* by the *elav-*

GAL4 line in both *robo*^{3} and *robo*^{5} homozygotes rescued the midline crossing of Fas II positive axons including pCC and other identified neurons.

Robo Appears to Function in a Cell Autonomous Fashion. To test whether Robo can function in a cell autonomous fashion, we used the *UAS-robo* transgene with the *ftz*$_{ng}$*-GAL4* line (Lin et al., 1994) . The *ftz*$_{ng}$*-GAL4* line expresses in a subset of CNS neurons, including many of the earliest neurons to be affected by the *robo* mutation such as pCC, vMP2, dMP2, and MP1. Expression of *robo* by the *ftz*$_{ng}$*-GAL4* line is sufficient to rescue these identified neurons in the *robo* mutant: pCC, which in robo mutants heads towards and crosses the midline, in these rescued embryos now projects ipsilaterally and does not cross the midline. When the same embryos were stained with the anti-robo MAb 13C9, we observed that all Robo-positive axons did not cross the midline. The *ftz*$_{ng}$*-GAL4* line drives expression in many of the axons in the pCC pathway (Lin et al., 1994), a medial longitudinal fascicle. In *robo* mutants, this axon fascicle freely crosses and circles the midline, joining with its contralateral pathway. When rescued by the *ftz*$_{ng}$*-GAL4* line driving UAS-*robo*, this pathway now largely remains on its own side of the midline, even though occasionally a few axons cross the midline. These experiments support the notion that Robo can function in a cell autonomous fashion.

Expression of Mammalian *robo1* in the Rat Spinal Cord. The isolation of several vertebrate Robo homologues suggests that Robo may play a similar role in orchestrating midline crossing in the vertebrate nervous system as it does in Drosophila. In the vertebrate spinal cord, the ventral midline is comprised of a unique group of cells called the floor plate (for review, Colamarino and Tessier-Lavigne, 1995). As in the Drosophila nervous system, the vertebrate spinal cord contains both crossing and non-crossing axons. Spinal commissural neurons are born in the dorsal half of the spinal cord; commissural axons project to and cross the floor plate before turning longitudinally in a rostral direction. In contrast, the axons of two other classes of neurons, dorsal association neurons and ventral motor neurons, do not cross the floor plate (Altman and Bayer, 1984).

To address the possibility that Robo may play a role in organizing the projections of these spinal neurons, we examined the expression of rat *robo1* by RNA in situ hybridization. A rat *robo1* riboprobe spanning the first three Ig domains was hybridized to transverse sections of E13 rat spinal cord. At E13, when many commissural axons will have already extended across the floor plate (Altman and Bayer, 1984), rat *robo1* is expressed at high levels

in the dorsal spinal cord, in a pattern corresponding to the cell bodies of commissural neurons. Rat *robo1* is also expressed at lower levels in a subpopulation of ventral cells in the region of the developing motor column. Interestingly, this expression pattern is similar to and overlaps partly with the mRNA encoding DCC, another Ig superfamily member which is also expressed on commissural and motor neurons and encodes a receptor for Netrin-1 (Keino-Masu et al, 1996). Rat *robo1* is not, however, expressed in the either the floor plate or the roof plate of the spinal cord or in the dorsal root ganglia. This is in contrast to rat *cdo*, which is strongly expressed in the roof plate (KB, MT-L, and R. Krauss. In the periphery, rat *robo1* is also found to be expressed in the the myotome and developing limb, in a pattern reminiscent of *c-met* (Ebens et al, 1996), indicating that rat *robo1* may also be expressed by migrating muscle precursor cells. Therefore, like its Drosophila homologue, rat *roboI* RNA is expressed by both crossing and non-crossing populations of axons, indicating that it encodes the functional equivalent of D-Robo1.

Genetic Stocks. All eight independent *robo* alleles were isolated on chromosomes deficient for *Fasciclin III* as described in Seeger et al., 1993. Subsequent use of a duplication that includes *FasIII*, and recombination of the *robo* chromosomes, indicates that the *robo* phenotype is independent of the absence of *FasIII*. Deficiencies were obtained from the Drosophila stock center at Bloomington, Indiana.

Cloning and Molecular Analysis of the *robo* Genes. Start points for a molecular walk to *robo* were obtained from the Berkeley and Crete Drosophila Genome Projects. Chromosomal walking was performed using standard techniques to isolate cosmids from the Tamkun library (Tamkun et al., 1992). cDNAs were isolated from the Zinn 9-12 hour Drosophila embryo gt11 library (Zinn et al., 1988), and from a human fetal brain library (Stratagene). Northern blot of poly-A^+ RNA and reverse Northern blots were hybridized using sensitive Church conditions.

Sequencing of the cDNAs and genomic subclones was performed by the dideoxynucleotide chain termination method using Sequenase (USB) following the manufacturer's protocol and with the AutoRead kit or AutoCycle kit (Pharmacia) or by ^{33}P cycle sequencing. Reactions were analyzed on a Pharmacia LKB or ABI automated laser fluorescent DNA sequencers respectively. The cDNAs were sequenced completely on both strands. Sequence contigs were compiled using Lasergene, Intelligenetics, and AssemblyLIGN software (Kodak Eastman). Database searches were performed using BLAST

(Altschuel et al., 1990).

A full length *D-robo1* cDNA was generated by ligating two partial cDNAs at an internal HpaI site and subcloning into the EcoRI site of pBluescript.SK+. A full length *H-robo1* cDNA was synthesized by ligating an XbaI-SalI fragment from a cDNA and a PCR product coding for the carboxy-terminal 222 amino acids at a SalI site. The PCR product has an EcoRI site introduced at the stop codon. The ligation product was cloned into pBluescript.SK+ digested with XbaI and EcoRI.

To clone the rat *robo1* cDNA, degenerate oligonucleotide primers designed against sequences conserved between the 5' ends of D-Robo1 and H-Robo1 were used to amplify a 500 bp fragment from an E13 rat brain cDNA by PCR. This fragment was used to screen an E13 spinal cord library at high stringency, resulting in the isolation of a 4.2 kb cDNA clone comprising all but the last 700 nucleotides. Subsequent screenings of the library with non-overlapping probes from this cDNA led to the isolation of 4 partial and 7 full length clones. To clone the rat *robo2* cDNA, we screened the same library with a fragment of the *H-robo2* cDNA.

Expressed Sequence Tag and Genomic Sequences. The ESTs yu23d11 (#H77734), zr54g12 (#AA236414) and yq76e12 (#H52936, #H52937) code for portions of H-RoboI. The EST yq7e12 is aberrantly spliced to part of the human glycophorinB gene. Five ESTs yn50a07, yg02b06, yg17b06, yn13a04 and ym17g11 code for part of *H-robo2*. The Drosophila P1 clone DS00329 encodes the genomic sequence of *D-robo2*. Sequences 1825710 and 1825711 (both: #U88183; locus ZK377) code for the predicted sequence of C. elegans *robo*. The EST vi62e02 (#AA499193) codes for mouse *robo1*.

Identification of Molecular Defects In *robo* Alleles. Southern blots of *robo* alleles and their parental chromosomes were hybridized with fragments from the genomic cosmid clone 106-1435 or partial cDNA clones to identify restriction fragment length polymorphisms affecting the *robo* transcription unit. DNA was obtained from homozygous mutant embryos. 35 cycles of the PCR was subsequently performed on the DNA obtained from half an embryo. Primers specific for the region flanking the CfoI polymorphism used were : ROBO6 (5'-GCATTGGGTCATCTGTAGAG -3') and ROBO23 (5'-AGCTATCTGGAGGGAGGCAT-3'). The PCR products were purified on a Pharmacia H300 spin column and sequenced directly.

Transformation of Drosophila, *robo* Rescue, and Overexpression. The 16 kb XbaI

fragment from cosmid 106-1435 was cloned into the Drosophila transformation vector pCaSpeR3. Transformant lines were generated and mapped by standard procedures. Four independent lines were shown to rescue *robo*^{1,3,5} alleles as judged by MAb 1D4 staining.

PCR amplification of the D-robo ORF using the primers (5'-GAGTGGTGAATTCAACAGCACCAAAACCACAAAATGCATCCC-3') and (5'-CGGGGAGTCTAGAACACTTCATCCTTAGGTG-3') produced a PCR product with an altered ribosome binding site that more closely matches the Drosophila consensus (Cavener, 1987), and has only 21bp of 5' UTR and no 3' UTR sequences. The PCR product was digested with EcoRI and XbaI and cloned into pBluescript (Stratagene) and subsequently, pUAST (Brand and Perrimon 1993). Transformant lines were crossed to *elav-GAL4* and *sca-GAL4* lines which express GAL4 in all neurons, or *ftzng-GAL4* which expresses in a subset of CNS neurons (Lin et al, 1994). Embryos were assayed by staining with MAbs BP102, 1D4 and 13C9. For ectopic expression in the *robo* mutant background, the stocks *robo*^{3} and *robo*^{5} (both protein nulls) were used. Crosses utilized the stocks *w; robo/CyO; UAS-robo* and *w; robo/CyO; elav-GAL4*. Due to the difficulty of maintaining a balanced stock, *robo/+; ftz-ngGAL4/+* males were generated as required.

Generation of Fusion Proteins and Antibodies. A six histidine tagged fusion protein was constructed by cloning amino acids 404-725 of the D-robo protein into the PstI site of the pQE31 vector (Qiagen). Fusion proteins were purified under denaturing conditions and subsequently dialyzed against PBS. Immunization of mice and MAb production followed standard protocols (Patel, 1994).

RNA Localization and Protein Immunocytochemistry. Digoxigenin labeled antisense *robo* transcripts were generated from a subclone of a *robo* cDNA in Bluescript. In-situ tissue hybridization was performed as described in Tear et al., 1996. Immunocytochemistry was performed as described by Patel, 1994. MAb 1D4 was used at a dilution of 1:5 and BP102 at 1:10. For anti-robo staining, MAb 13C9 was diluted 1:10 in PBS with 0.1% Tween-20, and the embryos were fixed and cracked so as to minimize exposure to methanol. The presence of triton and storage of embryos in methanol were both found to destroy the activity of MAb 13C9.

In situ hybridization of rat spinal cords was carried out essentially as described in Fan and Tessier-Lavigne, 1994. E13 embryos were fixed in 4% paraformaldehyde, processed, embedded in OCT, and sectioned to 10 m. A 1.0kb ^{35}S antisense rRobo riboprobe spannning

the the first three immunoglobulin domains was used for hybridization. An additional non-overlapping probe was also used with identical results. DCC transcripts were detected as described in Keino-Masu et al., 1996. Immunohistochemistry against TAG-1 was carried out on 10 m transverse spinal cord sections using 4D7 monoclonal antibody (Dodd et al, 1988).

Electron Microscopy. Canton S embryos were hand devitellinized, opened dorsally to remove the gut, and prepared for immunoelectron microscopy according to the procedures described previously (Lin et al., 1994), with the following modifications. The fixed embryos were incubated sequentially with MAb 13C9 (1:1) for 1-2 hours, biotinylated goat anti-mouse secondary antibody (1:250) for 1.5 hours, and then streptavidin-conjugated HRP (1:200) for 1.5 hours. Hydrogen peroxide (0.01%) was used instead of glucose oxidase for the HRP-DAB reaction.

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All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(v) COMPUTER READABLE FORM:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
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(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGCATCCCA TGCATCCCGA AAACCACGCC ATCGCCCGGA GCACGAGCAC CACTAATAAC 60

CCATCTCGCA GTCGGAGCAG CAGGATGTGG CTCCTGCCCG CCTGGCTGCT CCTCGTCCTG 120

GTGGCCAGCA ATGGCCTGCC AGCAGTCAGA GGCCAGTACC AATCGCCACG TATCATCGAG 180

CATCCCACGG ATCTGGTCGT TAAGAAGAAT GAACCCGCCA CGCTCAACTG CAAAGTGGAG 240

GGCAAGCCGG AACCCACCAT TGAGTGGTTT AAGGATGGCG AACCCGTCAG CACCAACGAA 300

AAGAAATCGC ACCGCGTCCA GTTCAAGGAC GGCGCCCTCT TCTTTTACAG GACAATGCAA 360

GGCAAGAAGG AGCAGGACGG CGGAGAGTAC TGGTGCGTGG CCAAGAACCG AGTGGGCCAG 420

GCCGTTAGTC GCCATGCCTC CCTCCAGATA GCTGTTTTGC GCGACGATTT TCGCGTGGAG 480

CCCAAAGACA CGCGAGTGGC CAAAGGCGAG ACGGCTCTGC TGGAGTGTGG GCCGCCCAAA 540

GGCATTCCAG AGCCAACGCT GATTTGGATA AAGGACGGCG TTCCCTTGGA CGACCTGAAA 600

GCCATGTCGT TTGGCGCCAG CTCCCGCGTT CGAATTGTGG ACGGTGGCAA CCTGCTGATC 660

AGCAATGTGG AGCCCATTGA TGAGGGCAAC TACAAGTGCA TTGCCCAGAA TCTGGTAGGC 720

ACCCGCGAGA GCAGCTATGC CAAGCTGATT GTCCAGGTCA AACCATACTT TATGAAGGAG 780

CCCAAGGATC AGGTGATGCT CTACGGCCAG ACAGCCACTT TCCACTGCTC AGTGGGCGGT 840

GATCCGCCGC CGAAAGTGTT GTGGAAAAAG GAGGAGGGCA ATATTCCGGT GTCCAGAGCG 900

CGAATCCTTC ACGACGAGAA AAGTTTAGAG ATATCCAACA TAACGCCCAC CGATGAGGGC 960

ACCTATGTCT GCGAGGCACA CAACAATGTC GGTCAGATCA GCGCTAGGGC TTCTCTTATA 1020

GTCCACGCTC CGCCGAACTT TACGAAAAGA CCCAGTAACA AGAAAGTGGG ACTAAATGGG 1080

GTTGTCCAAC TACCTTGCAT GGCCTCCGGA AACCCTCCGC CGTCTGTATT CTGGACCAAG 1140

GAAGGAGTAT CCACTCTTAT GTTCCCAAAT AGTTCGCACG GAAGGCAGTA TGTGGCTGCC 1200

GATGGAACTC TGCAGATTAC GGATGTGCGG CAGGAAGACG AAGGCTACTA TGTGTGTTCC 1260

GCTTTCAGTG TAGTCGATTC CTCTACAGTA CGGGTTTTCC TGCAAGTCAG CTCGGTAGAC 1320

GAGCGTCCAC CTCCGATTAT TCAAATCGGA CCTGCCAATC AAACACTGCC CAAGGGATCA 1380

GTTGCTACTT TACCCTGTCG GGCCACTGGA AATCCCAGTC CCCGTATCAA GTGGTTCCAC 1440

GATGGACATG CCGTACAAGC GGGCAATCGA TACAGCATCA TCCAAGGAAG CTCACTGAGA 1500

GTCGATGACC TTCAACTAAG TGACTCTGGT ACCTACACCT GCACTGCATC TGGCGAACGA 1560

GGAGAAACTT CCTGGGCTGC CACACTAACG GTGGAAAAAC CCGGTTCTAC ATCTCTTCAC 1620

CGGGCAGCTG ATCCTAGCAC TTATCCTGCT CCTCCAGGAA CACCTAAAGT CCTGAATGTC 1680

AGTCGCACCA GCATTAGTCT TCGTTGGGCT AAAAGCCAAG AGAAACCCGG AGCTGTGGGC 1740

CCAATCATTG GATACACTGT AGAGTACTTC AGTCCGGATC TGCAAACTGG TTGGATTGTG 1800

GCTGCCCATC GAGTCGGCGA CACTCAAGTC ACTATCTCGG GTCTCACTCC TGGCACTTCG 1860

TATGTGTTCC TAGTTAGAGC TGAGAATACT CAGGGTATTT CTGTGCCTTC CGGCTTATCA 1920

AATGTTATTA AAACCATTGA GGCAGATTTC GATGCAGCTT CTGCCAATGA TTTGTCAGCA 1980

GCTCGAACTT TGCTGACAGG AAAGTCGGTG GAGCTAATAG ATGCCTCGGC TATCAATGCT 2040

AGTGCCGTTA GACTTGAGTG GATGCTCCAC GTGAGCGCTG ATGAGAAATA CGTAGAGGGC 2100

CTGCGCATAC ACTATAAGGA TGCCAGTGTA CCATCCGCAC AGTATCACTC GATCACTGTT 2160

ATGGATGCCT CTGCAGAATC GTTTGTGGTG GGAAACCTTA AGAAGTACAC CAAGTATGAG 2220

TTCTTCCTAA CACCCTTTTT TGAGACAATT GAAGGACAGC CCAGTAACTC CAAGACAGCC 2280

CTCACCTATG AAGATGTTCC CTCCGCACCA CCGGATAACA TTCAGATTGG CATGTACAAC 2340

CAAACAGCCG GTTGGGTGCG TTGGACTCCG CCACCCTCCC AGCACCACAA TGGCAATTTG 2400

TATGGCTACA AGATTGAGGT CAGCGCCGGT AACACCATGA AGGTGCTGGC CAATATGACT 2460

CTTAATGCTA CCACCACATC TGTGCTCCTA AATAACCTAA CCACCGGAGC TGTGTACAGC 2520

GTGAGGTTGA ACTCCTTTAC CAAGGCAGGA GATGGACCTT ACTCCAAACC GATATCACTA 2580

TTCATGGACC CCACCCATCA TGTGCATCCG CCACGGGCAC ATCCAAGCGG CACCCATGAT 2640

GGGCGACATG AGGGACAGGA TCTCACGTAT CATAACAATG GCAACATACC ACCTGGCGAC 2700

ATTAATCCCA CCACTCATAA AAAGACCACT GACTACCTAT CTGGACCGTG GCTAATGGTG 2760

CTGGTCTGCA TCGTTCTTCT AGTCCTGGTT ATTTCGGCGG CTATTTCGAT GGTCTACTTC 2820

AAGCGCAAGC ATCAAATGAC CAAGGAATTG GGTCACTTAA GTGTGGTCAG TGACAACGAA 2880

ATAACCGCAT TAAATATCAA TAGCAAAGAG AGCCTTTGGA TAGACCATCA TCGTGGATGG 2940

CGAACTGCCG ATACTGACAA AGACTCAGGA TTAAGCGAAT CGAAGCTACT ATCCCACGTT 3000

AACAGCAGTC AATCCAACTA CAATAACTCC GATGGAGGAA CCGATTATGC AGAAGTTGAC 3060

ACCCGTAACC TTACCACCTT CTACAATTGT CGCAAGAGCC CCGATAATCC CACGCCGTAC 3120

GCCACCACTA TGATCATTGG TACCTCTTCC AGTGAGACCT GCACCAAGAC AACATCTATA 3180

AGTGCCGATA AGGACTCGGG AACTCATTCG CCCTATTCTG ACGCATTTGC CGGTCAGGTG 3240

CCAGCGGTTC CTGTTGTCAA ATCCAACTAT CTTCAGTATC CGGTTGAACC GATCAACTGG 3300

TCAGAGTTTC TACCCCCGCC GCCAGAACAC CCACCTCCGT CTTCTACCTA TGGATACGCA 3360

CAAGGATCTC CTGAATCTTC GCGGAAGAGC TCCAAAAGCG CAGGTTCCGG CATTTCTACA 3420

AATCAAAGCA TTCTGAACGC ATCCATACAC AGCAGCTCCT CGGGCGGCTT TTCAGCTTGG 3480

GGAGTATCGC CCCAATATGC TGTCGCCTGT CCACCGGAAA ACGTTTATAG CAATCCGCTG 3540

TCGGCAGTGG CTGGCGGCAC CCAGAACCGC TATCAGATAA CGCCCACAAA CCAACATCCG 3600

CCACAGTTAC CGGCCTACTT TGCCACCACG GGTCCAGGAG GAGCTGTACC ACCCAACCAC 3660

CTGCCATTTG CCACACAGCG TCATGCAGCC AGCGAGTACC AGGCTGGACT GAATGCAGCG 3720

CGATGTGCCC AAAGCCGCGC CTGCAACAGC TGCGATGCCT TGGCCACACC CTCGCCCATG 3780

CAACCCCCAC CGCCAGTTCC CGTACCCGAG GGCTGGTACC AACCGGTGCA TCCCAATAGC 3840

CACCCGATGC ACCCGACCTC CTCCAACCAC CAGATCTACC AGTGCTCCTC CGAGTGCTCG 3900

GATCACTCGA GGAGCTCGCA GAGTCACAAG CGGCAGCTGC AGCTCGAGGA GCACGGCAGC 3960

AGTGCCAAAC AACGCGGAGG ACACCACCGT CGACGAGCCC CGGTGGTGCA GCCGTGCATG 4020

GAGAGCGAGA ACGAGAACAT GCTGGCGGAG TACGAGCAGC GCCAGTACAC CAGCGATTGC 4080

TGCAATAGCT CCCGCGAGGG CGACACCTGC TCCTGCAGCG AGGGATCCTG TCTTTACGCC 4140

GAGGCGGGCG AGCCGGCGCC TCGTCAAATG ACTGCTAAGA ACACCTAA 4188

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1395 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met His Pro Met His Pro Glu Asn His Ala Ile Ala Arg Ser Thr Ser
1               5                  10                  15
Thr Thr Asn Asn Pro Ser Arg Ser Arg Ser Ser Arg Met Trp Leu Leu
            20                  25                  30
Pro Ala Trp Leu Leu Leu Val Leu Val Ala Ser Asn Gly Leu Pro Ala
        35                  40                  45
Val Arg Gly Gln Tyr Gln Ser Pro Arg Ile Ile Glu His Pro Thr Asp
    50                  55                  60
Leu Val Val Lys Lys Asn Glu Pro Ala Thr Leu Asn Cys Lys Val Glu
65                  70                  75                  80
Gly Lys Pro Glu Pro Thr Ile Glu Trp Phe Lys Asp Gly Glu Pro Val
                85                  90                  95
Ser Thr Asn Glu Lys Lys Ser His Arg Val Gln Phe Lys Asp Gly Ala
            100                 105                 110
Leu Phe Phe Tyr Arg Thr Met Gln Gly Lys Lys Glu Gln Asp Gly Gly
        115                 120                 125
Glu Tyr Trp Cys Val Ala Lys Asn Arg Val Gly Gln Ala Val Ser Arg
    130                 135                 140
His Ala Ser Leu Gln Ile Ala Val Leu Arg Asp Asp Phe Arg Val Glu
145                 150                 155                 160
Pro Lys Asp Thr Arg Val Ala Lys Gly Glu Thr Ala Leu Leu Glu Cys
                165                 170                 175
Gly Pro Pro Lys Gly Ile Pro Glu Pro Thr Leu Ile Trp Ile Lys Asp
            180                 185                 190
Gly Val Pro Leu Asp Asp Leu Lys Ala Met Ser Phe Gly Ala Ser Ser
        195                 200                 205
Arg Val Arg Ile Val Asp Gly Gly Asn Leu Leu Ile Ser Asn Val Glu
    210                 215                 220
Pro Ile Asp Glu Gly Asn Tyr Lys Cys Ile Ala Gln Asn Leu Val Gly
225                 230                 235                 240
Thr Arg Glu Ser Ser Tyr Ala Lys Leu Ile Val Gln Val Lys Pro Tyr
                245                 250                 255
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Phe Met Lys Glu Pro Lys Asp Gln Val Met Leu Tyr Gly Gln Thr Ala
260 265 270
Thr Phe His Cys Ser Val Gly Gly Asp Pro Pro Pro Lys Val Leu Trp
275 280 285
Lys Lys Glu Glu Gly Asn Ile Pro Val Ser Arg Ala Arg Ile Leu His
290 295 300
Asp Glu Lys Ser Leu Glu Ile Ser Asn Ile Thr Pro Thr Asp Glu Gly
305 310 315 320
Thr Tyr Val Cys Glu Ala His Asn Asn Val Gly Gln Ile Ser Ala Arg
325 330 335
Ala Ser Leu Ile Val His Ala Pro Pro Asn Phe Thr Lys Arg Pro Ser
340 345 350
Asn Lys Lys Val Gly Leu Asn Gly Val Val Gln Leu Pro Cys Met Ala
355 360 365
Ser Gly Asn Pro Pro Pro Ser Val Phe Trp Thr Lys Glu Gly Val Ser
370 375 380
Thr Leu Met Phe Pro Asn Ser Ser His Gly Arg Gln Tyr Val Ala Ala
385 390 395 400
Asp Gly Thr Leu Gln Ile Thr Asp Val Arg Gln Glu Asp Glu Gly Tyr
405 410 415
Tyr Val Cys Ser Ala Phe Ser Val Val Asp Ser Ser Thr Val Arg Val
420 425 430
Phe Leu Gln Val Ser Ser Val Asp Glu Arg Pro Pro Pro Ile Ile Gln
435 440 445
Ile Gly Pro Ala Asn Gln Thr Leu Pro Lys Gly Ser Val Ala Thr Leu
450 455 460
Pro Cys Arg Ala Thr Gly Asn Pro Ser Pro Arg Ile Lys Trp Phe His
465 470 475 480
Asp Gly His Ala Val Gln Ala Gly Asn Arg Tyr Ser Ile Ile Gln Gly
485 490 495
Ser Ser Leu Arg Val Asp Asp Leu Gln Leu Ser Asp Ser Gly Thr Tyr
500 505 510
Thr Cys Thr Ala Ser Gly Glu Arg Gly Glu Thr Ser Trp Ala Ala Thr
515 520 525
Leu Thr Val Glu Lys Pro Gly Ser Thr Ser Leu His Arg Ala Ala Asp
530 535 540
Pro Ser Thr Tyr Pro Ala Pro Pro Gly Thr Pro Lys Val Leu Asn Val
545 550 555 560

Ser Arg Thr Ser Ile Ser Leu Arg Trp Ala Lys Ser Gln Glu Lys Pro
565 570 575
Gly Ala Val Gly Pro Ile Ile Gly Tyr Thr Val Glu Tyr Phe Ser Pro
580 585 590
Asp Leu Gln Thr Gly Trp Ile Val Ala Ala His Arg Val Gly Asp Thr
595 600 605
Gln Val Thr Ile Ser Gly Leu Thr Pro Gly Thr Ser Tyr Val Phe Leu
610 615 620
Val Arg Ala Glu Asn Thr Gln Gly Ile Ser Val Pro Ser Gly Leu Ser
625 630 635 640
Asn Val Ile Lys Thr Ile Glu Ala Asp Phe Asp Ala Ala Ser Ala Asn
645 650 655
Asp Leu Ser Ala Ala Arg Thr Leu Leu Thr Gly Lys Ser Val Glu Leu
660 665 670
Ile Asp Ala Ser Ala Ile Asn Ala Ser Ala Val Arg Leu Glu Trp Met
675 680 685
Leu His Val Ser Ala Asp Glu Lys Tyr Val Glu Gly Leu Arg Ile His
690 695 700
Tyr Lys Asp Ala Ser Val Pro Ser Ala Gln Tyr His Ser Ile Thr Val
705 710 715 720
Met Asp Ala Ser Ala Glu Ser Phe Val Val Gly Asn Leu Lys Lys Tyr
725 730 735
Thr Lys Tyr Glu Phe Phe Leu Thr Pro Phe Phe Glu Thr Ile Glu Gly
740 745 750
Gln Pro Ser Asn Ser Lys Thr Ala Leu Thr Tyr Glu Asp Val Pro Ser
755 760 765
Ala Pro Pro Asp Asn Ile Gln Ile Gly Met Tyr Asn Gln Thr Ala Gly
770 775 780
Trp Val Arg Trp Thr Pro Pro Pro Ser Gln His His Asn Gly Asn Leu
785 790 795 800
Tyr Gly Tyr Lys Ile Glu Val Ser Ala Gly Asn Thr Met Lys Val Leu
805 810 815
Ala Asn Met Thr Leu Asn Ala Thr Thr Thr Ser Val Leu Leu Asn Asn
820 825 830
Leu Thr Thr Gly Ala Val Tyr Ser Val Arg Leu Asn Ser Phe Thr Lys
835 840 845
Ala Gly Asp Gly Pro Tyr Ser Lys Pro Ile Ser Leu Phe Met Asp Pro
850 855 860

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Thr His His Val His Pro Pro Arg Ala His Pro Ser Gly Thr His Asp
865                 870                 875                 880
Gly Arg His Glu Gly Gln Asp Leu Thr Tyr His Asn Asn Gly Asn Ile
                885                 890                 895
Pro Pro Gly Asp Ile Asn Pro Thr Thr His Lys Lys Thr Thr Asp Tyr
            900                 905                 910
Leu Ser Gly Pro Trp Leu Met Val Leu Val Cys Ile Val Leu Leu Val
        915                 920                 925
Leu Val Ile Ser Ala Ala Ile Ser Met Val Tyr Phe Lys Arg Lys His
    930                 935                 940
Gln Met Thr Lys Glu Leu Gly His Leu Ser Val Val Ser Asp Asn Glu
945                 950                 955                 960
Ile Thr Ala Leu Asn Ile Asn Ser Lys Glu Ser Leu Trp Ile Asp His
                965                 970                 975
His Arg Gly Trp Arg Thr Ala Asp Thr Asp Lys Asp Ser Gly Leu Ser
            980                 985                 990
Glu Ser Lys Leu Leu Ser His Val Asn Ser Ser Gln Ser Asn Tyr Asn
        995                 1000                1005
Asn Ser Asp Gly Gly Thr Asp Tyr Ala Glu Val Asp Thr Arg Asn Leu
    1010                1015                1020
Thr Thr Phe Tyr Asn Cys Arg Lys Ser Pro Asp Asn Pro Thr Pro Tyr
1025                1030                1035                1040
Ala Thr Thr Met Ile Ile Gly Thr Ser Ser Ser Glu Thr Cys Thr Lys
                1045                1050                1055
Thr Thr Ser Ile Ser Ala Asp Lys Asp Ser Gly Thr His Ser Pro Tyr
            1060                1065                1070
Ser Asp Ala Phe Ala Gly Gln Val Pro Ala Val Pro Val Val Lys Ser
        1075                1080                1085
Asn Tyr Leu Gln Tyr Pro Val Glu Pro Ile Asn Trp Ser Glu Phe Leu
    1090                1095                1100
Pro Pro Pro Pro Glu His Pro Pro Pro Ser Ser Thr Tyr Gly Tyr Ala
1105                1110                1115                1120
Gln Gly Ser Pro Glu Ser Ser Arg Lys Ser Ser Lys Ser Ala Gly Ser
                1125                1130                1135
Gly Ile Ser Thr Asn Gln Ser Ile Leu Asn Ala Ser Ile His Ser Ser
            1140                1145                1150
Ser Ser Gly Gly Phe Ser Ala Trp Gly Val Ser Pro Gln Tyr Ala Val
        1155                1160                1165
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Ala Cys Pro Pro Glu Asn Val Tyr Ser Asn Pro Leu Ser Ala Val Ala
1170 1175 1180
Gly Gly Thr Gln Asn Arg Tyr Gln Ile Thr Pro Thr Asn Gln His Pro
1185 1190 1195 1200
Pro Gln Leu Pro Ala Tyr Phe Ala Thr Thr Gly Pro Gly Gly Ala Val
1205 1210 1215
Pro Pro Asn His Leu Pro Phe Ala Thr Gln Arg His Ala Ala Ser Glu
1220 1225 1230
Tyr Gln Ala Gly Leu Asn Ala Ala Arg Cys Ala Gln Ser Arg Ala Cys
1235 1240 1245
Asn Ser Cys Asp Ala Leu Ala Thr Pro Ser Pro Met Gln Pro Pro Pro
1250 1255 1260
Pro Val Pro Val Pro Glu Gly Trp Tyr Gln Pro Val His Pro Asn Ser
1265 1270 1275 1280
His Pro Met His Pro Thr Ser Ser Asn His Gln Ile Tyr Gln Cys Ser
1285 1290 1295
Ser Glu Cys Ser Asp His Ser Arg Ser Ser Gln Ser His Lys Arg Gln
1300 1305 1310
Leu Gln Leu Glu Glu His Gly Ser Ser Ala Lys Gln Arg Gly Gly His
1315 1320 1325
His Arg Arg Arg Ala Pro Val Val Gln Pro Cys Met Glu Ser Glu Asn
1330 1335 1340
Glu Asn Met Leu Ala Glu Tyr Glu Gln Arg Gln Tyr Thr Ser Asp Cys
1345 1350 1355 1360
Cys Asn Ser Ser Arg Glu Gly Asp Thr Cys Ser Cys Ser Glu Gly Ser
1365 1370 1375
Cys Leu Tyr Ala Glu Ala Gly Glu Pro Ala Pro Arg Gln Met Thr Ala
1380 1385 1390
Lys Asn Thr
1395

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTGAAAATC CACGCATCAT CGAGCATCCC ATGGACACGA CGGTGCCAAA AAATGATCCA 60

TTTACGTTTA ATTGCCAGGC CGAGGGCAAT CCAACACCAA CCATTCAATG GTTTAAGGAC 120

GGTCGCGAAC TGAAGACGGA TACGGGTTCG CATCGCATAA TGCTGCCCGC CGGGGGTCTA 180

TTCTTTCTCA AGGTTATCCA CTCACGTAGA GAGAGCGATG CGGGCACTTA CTGGTGCGAG 240

GCCAAAAACG AGTTTGGAGT GGCACGGTCC AGGAATGCAA CGTTGCAAGT GGCAGTTCTC 300

CGCGACGAAT TCCGTTTGGA GCCGGCAAAT ACCCGCGTGG CCCAAGGCGA GGTGGCCCTG 360

ATGGAATGCG GTGCCCCCCG AGGATCTCCG GAGCCGCAAA TCTCGTGGCG CAAGAACGGC 420

CAGACCCTGA ATCTTGTCGG GAACAAGCGG ATTCGCATTG TCGACGGTGG CAATCTGGCC 480

ATCCAGGAAG CCCGCCAATC GGACGACGGA CGCTACCAGT GTGTGGTCAA GAATGTGGTT 540

GGCACCCGGG AGTCGGCCAC CGCTTTTCTT AAAGTGCATG TACGTCCATT CCTCATCCGA 600

GGACCCCAGA ATCAGACGGC GGTGGTGGGC AGCTCGGTGG TCTTCCAGTG CCGCATCGGA 660

GGCGATCCCC TGCCTGATGT CCTGTGGCGA CGCACTGCCT CCGGCGGCAA TATGCCACTG 720

CGTAAGTTTT CTTGGCTTCA TTCAGCTTCA GGTCGTGTGC ACGTACTTGA GGACCGCAGT 780

CTGAAGCTGG ACGACGTTAC TCTGGAGGAC ATGGGCGAGT ACACTTGCGA GGCGGACAAT 840

GCGGTGGGCG GCATCACGGC CACTGGCATC CTCACCGTTC ACGCTCCCCC CAAATTTGTG 900

ATACGCCCCA AGAATCAGCT GGTGGAGATC GGTGATGAAG TGCTGTTCGA GTGCCAAGCG 960

AATGGACATC CCCGACCAAC GCTCTACTGG TCGGTGGAGG GCAACAGCTC CCTGCTGCTC 1020

CCCGGCTATC GGGATGGCCG CATGGAAGTG ACCCTGACGC CCGAGGGGCG CTCGGTGCTC 1080

TCGATAGCTC GATTTGCCCG TGAGGATTCC GGAAAGGTGG TCACTTGCAA CGCCCTGAAC 1140

GCCGTGGGCA GCGTCAGCAG TCGGACTGTG GTCAGTGTGG ATACGCAATT CGAGCTGCCA 1200

CCGCCGATTA TCGAACAGGG GCCCGTGAAT CAAACGTTGC CCGTTAAATC AATTGTGGTT 1260

CTGCCATGCC GAACTCTGGG CACTCCAGTG CCACAGGTCT CTTGGTACCT GGATGGCATA 1320

CCCATCGATG TGCAGGAGCA CGAGCGGCGG AATCTTTCGG ACGCTGGAGC CTTAACCATT 1380

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GGAAAATCCT CTTGGAGTGG TTACCTTCGT CTGGACACCC CGACAAATCC GAATATCAAG 1500

TTCTTCAGAG CCCCAGAACT TTCCACCTAC CCAGGGCCGC CAGGAAAACC GCAAATGGTG 1560

GAGAAGGGCG AAAATTCGGT GACTCTCAGC TGGACGAGGA GCAACAAGGT GGGCGGCTCC 1620

AGTCTGGTGG GCTATGTAAT CGAGATGTTT GGCAAAAACG AAACGGATGG CTGGGTGGCT 1680

GTGGGCACTA GGGTGCAAAA TACCACGTTT ACCCAAACGG GTCTGCTGCC GGGTGTGAAT 1740

TACTTCTTTC TAATTCGAGC CGAGAACTCC CATGGCTTAT CACTGCCCAG TCCGATGTCG 1800

GAACCCATTA CGGTGGGAAC GCGCTACTTC AATAGTGGTC TGGATCTGAG CGAGGCTCGT 1860

GCCAGTCTGC TGTCCGGAGA TGTTGTGGAG CTGAGCAACG CCAGTGTGGT GGACTCCACT 1920

AGCATGAAAC TCACCTGGCA GATCATCAAT GGCAAATACG TCGAGGGCTT CTATGTCTAT 1980

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TCGACAAAGC CAAATATTGC AGCTGCCGGC AAACGTGATG GGGAGACAAA CCAGAGTGGA 2160

GGAGGAGCTC CGACCCCACT GAACACCAAG TATCGCATGC TAACGATTCT CAATGGCGGT 2220

GGCGCCTCAT CCTGCACCAT CACCGGGCTC GTCCAGTACA CGCTGTATGA ATTTTTCATC 2280

GTGCCATTTT ACAAATCCGT CGAGGGCAAG CCGTCGAATT CGCGCATCGC TCGCACCCTT 2340

GAAGATGTTC CCTCTGAGGC ACCATATGGA ATGGAGGCTC TGCTGTTGAA CTCCTCCGCG 2400

GTCTTCCTCA AATGGAAGGC ACCAGAACTC AAGGATCGGC ATGGTGTTCT CTTGAACTAT 2460

CATGTTATAG TCCGAGGTAT TGACACTGCC CACAATTTCT CACGCATTTT GACAAATGTC 2520

ACCATCGATG CCGCTTCGCC TACTCTGGTT TTGGCCAATC TCACCGAAGG CGTCATGTAC 2580

ACCGTGGGCG TGGCGGCCGG AAATAACGCT GGAGTTGGTC CTTATTGTGT CCCAGCTACT 2640

TTGCGTTTGG ATCCCATCAC AAAGCGACTC GATCCGTTCA TCAATCAGCG GGACCATGTT 2700

AACGATGTGC TGACGCAGCC CTGGTTCATA ATACTCCTGG GCGCCATCCT GGCCGTTCTT 2760

ATGCTGTCCT TTGGCGCAAT GGTCTTTGTG AAGCGCAAGC ACATGATGAT GAAGCAGTCG 2820

GCCCTAAATA CAATGCGTGG CAATCACACG AGCGACGTGC TCAAAATGCC GAGTCTATCG 2880

GCGCGCAATG GAAACGGCTA CTGGCTGGAC TCCTCCACCG GCGGAATGGT GTGGCGTCCC 2940

TCGCCCGGCG GCGACTCGCT GGAGATGCAA AAGGATCACA TCGCCGACTA TGCGCCGGTC 3000

TGCGGTGCCC CCGGTTCTCC GGCCGGCGGT GGCACCTCTT CCGGTGGATC CGGTGGCGCG 3060

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CAGCGGTACG TGGGCGAGTA CTCCAACATA CCGACCGACT ATGCAGAGGT GTCCAGTTTT 3180

GGCAAGGCAC CCAGCGAGTA TGGTCGGCAT GGCAACGCCT CCCCGGCCCC TTATGCCACC 3240

TCTTCGATCC TGAGTCCCCA CCAGCAGCAA CAGCAGCAGC AGCCGCGTTA TCAACAGCGA 3300

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CTGCCACCCA GCAACATCTA CCAGCAGATG TCCACCACCA GCGAGATATA CCCCACGAAC 3480

ACGGGTCCTT CGCGCTCTGT CTACTCTGAG CAGTATTACT ACCCCAAGGA CAAGCAGAGA 3540

CACATCCACA TCACCGAGAA CAAGCTGAGC AACTGCCACA CCTATGAGGC GGCTCCTGGC 3600

GCCAAGCAGT CCTCGCCGAT ATCCTCGCAG TTCGCCAGCG TGAGGCGGCA GCAGCTGCCG 3660

CCCAACTGCA GCATCGGCAG GGAAAGTGCC CGCTTCAAGG TGCTAAACAC GGATCAGGGC 3720

AAGAACCAGC AGAATCTCCT GGATCTCGAC GGCTCCTCGA TGTGCTACAA CGGTCTGGCA 3780

GACTCGGGCT GCGGTGGATC TCCCTCCCCG ATGGCCATGC TGATGTCGCA CGAGGACGAG 3840

CACGCGCTGT ACCACACGGC GGATGGGGAT CTGGACGACA TGGAACGACT GTACGTCAAG 3900

GTGGACGAGC AGCAGCCTCC ACAGCAGCAG CAGCAGCTGA TTCCCCTGGT CCCACAGCAT 3960

CCGGCGGAAG GTCACCTGCA GTCCTGGCGG AATCAGAGCA CGCGGAGCAG TCGGAAGAAC 4020

GGCCAGGAAT GCATCAAGGA ACCCAGCGAG TTGATCTACG CTCCGGGAAG CGTGGCCAGC 4080

GAACGGAGCC TCCTCAGCAA CTCGGGTAGC GGCACCAGCA GCCAGCCAGC TGGCCACAAT 4140

GTCTGA 4146

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1381 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Gly Glu Asn Pro Arg Ile Ile Glu His Pro Met Asp Thr Thr Val Pro
1               5                  10                  15
Lys Asn Asp Pro Phe Thr Phe Asn Cys Gln Ala Glu Gly Asn Pro Thr
            20                  25                  30
Pro Thr Ile Gln Trp Phe Lys Asp Gly Arg Glu Leu Lys Thr Asp Thr
        35                  40                  45
Gly Ser His Arg Ile Met Leu Pro Ala Gly Gly Leu Phe Phe Leu Lys
    50                  55                  60
Val Ile His Ser Arg Arg Glu Ser Asp Ala Gly Thr Tyr Trp Cys Glu
65                  70                  75                  80
Ala Lys Asn Glu Phe Gly Val Ala Arg Ser Arg Asn Ala Thr Leu Gln
                85                  90                  95
Val Ala Val Leu Arg Asp Glu Phe Arg Leu Glu Pro Ala Asn Thr Arg
            100                 105                 110
Val Ala Gln Gly Glu Val Ala Leu Met Glu Cys Gly Ala Pro Arg Gly
        115                 120                 125
Ser Pro Glu Pro Gln Ile Ser Trp Arg Lys Asn Gly Gln Thr Leu Asn
    130                 135                 140
Leu Val Gly Asn Lys Arg Ile Arg Ile Val Asp Gly Gly Asn Leu Ala
145                 150                 155                 160
Ile Gln Glu Ala Arg Gln Ser Asp Asp Gly Arg Tyr Gln Cys Val Val
                165                 170                 175
Lys Asn Val Val Gly Thr Arg Glu Ser Ala Thr Ala Phe Leu Lys Val
            180                 185                 190
His Val Arg Pro Phe Leu Ile Arg Gly Pro Gln Asn Gln Thr Ala Val
        195                 200                 205
Val Gly Ser Ser Val Val Phe Gln Cys Arg Ile Gly Gly Asp Pro Leu
    210                 215                 220
Pro Asp Val Leu Trp Arg Arg Thr Ala Ser Gly Gly Asn Met Pro Leu
225                 230                 235                 240
Arg Lys Phe Ser Trp Leu His Ser Ala Ser Gly Arg Val His Val Leu
                245                 250                 255
Glu Asp Arg Ser Leu Lys Leu Asp Asp Val Thr Leu Glu Asp Met Gly
            260                 265                 270
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Glu Tyr Thr Cys Glu Ala Asp Asn Ala Val Gly Gly Ile Thr Ala Thr
275 280 285
Gly Ile Leu Thr Val His Ala Pro Pro Lys Phe Val Ile Arg Pro Lys
290 295 300
Asn Gln Leu Val Glu Ile Gly Asp Glu Val Leu Phe Glu Cys Gln Ala
305 310 315 320
Asn Gly His Pro Arg Pro Thr Leu Tyr Trp Ser Val Glu Gly Asn Ser
325 330 335
Ser Leu Leu Leu Pro Gly Tyr Arg Asp Gly Arg Met Glu Val Thr Leu
340 345 350
Thr Pro Glu Gly Arg Ser Val Leu Ser Ile Ala Arg Phe Ala Arg Glu
355 360 365
Asp Ser Gly Lys Val Val Thr Cys Asn Ala Leu Asn Ala Val Gly Ser
370 375 380
Val Ser Ser Arg Thr Val Val Ser Val Asp Thr Gln Phe Glu Leu Pro
385 390 395 400
Pro Pro Ile Ile Glu Gln Gly Pro Val Asn Gln Thr Leu Pro Val Lys
405 410 415
Ser Ile Val Val Leu Pro Cys Arg Thr Leu Gly Thr Pro Val Pro Gln
420 425 430
Val Ser Trp Tyr Leu Asp Gly Ile Pro Ile Asp Val Gln Glu His Glu
435 440 445
Arg Arg Asn Leu Ser Asp Ala Gly Ala Leu Thr Ile Ser Asp Leu Gln
450 455 460
Arg His Glu Asp Glu Gly Leu Tyr Thr Cys Val Ala Ser Asn Arg Asn
465 470 475 480
Gly Lys Ser Ser Trp Ser Gly Tyr Leu Arg Leu Asp Thr Pro Thr Asn
485 490 495
Pro Asn Ile Lys Phe Phe Arg Ala Pro Glu Leu Ser Thr Tyr Pro Gly
500 505 510
Pro Pro Gly Lys Pro Gln Met Val Glu Lys Gly Glu Asn Ser Val Thr
515 520 525
Leu Ser Trp Thr Arg Ser Asn Lys Val Gly Gly Ser Ser Leu Val Gly
530 535 540
Tyr Val Ile Glu Met Phe Gly Lys Asn Glu Thr Asp Gly Trp Val Ala
545 550 555 560
Val Gly Thr Arg Val Gln Asn Thr Thr Phe Thr Gln Thr Gly Leu Leu
565 570 575

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Pro Gly Val Asn Tyr Phe Phe Leu Ile Arg Ala Glu Asn Ser His Gly
            580                 585                 590
Leu Ser Leu Pro Ser Pro Met Ser Glu Pro Ile Thr Val Gly Thr Arg
        595                 600                 605
Tyr Phe Asn Ser Gly Leu Asp Leu Ser Glu Ala Arg Ala Ser Leu Leu
    610                 615                 620
Ser Gly Asp Val Val Glu Leu Ser Asn Ala Ser Val Val Asp Ser Thr
625                 630                 635                 640
Ser Met Lys Leu Thr Trp Gln Ile Ile Asn Gly Lys Tyr Val Glu Gly
                645                 650                 655
Phe Tyr Val Tyr Ala Arg Gln Leu Pro Asn Pro Ile Val Asn Asn Pro
            660                 665                 670
Ala Pro Val Thr Ser Asn Thr Asn Pro Leu Leu Gly Ser Thr Ser Thr
        675                 680                 685
Ser Ala Ser Ala Ser Ala Ser Ala Ser Ala Leu Ile Ser Thr Lys Pro
    690                 695                 700
Asn Ile Ala Ala Ala Gly Lys Arg Asp Gly Glu Thr Asn Gln Ser Gly
705                 710                 715                 720
Gly Gly Ala Pro Thr Pro Leu Asn Thr Lys Tyr Arg Met Leu Thr Ile
                725                 730                 735
Leu Asn Gly Gly Gly Ala Ser Ser Cys Thr Ile Thr Gly Leu Val Gln
            740                 745                 750
Tyr Thr Leu Tyr Glu Phe Phe Ile Val Pro Phe Tyr Lys Ser Val Glu
        755                 760                 765
Gly Lys Pro Ser Asn Ser Arg Ile Ala Arg Thr Leu Glu Asp Val Pro
    770                 775                 780
Ser Glu Ala Pro Tyr Gly Met Glu Ala Leu Leu Leu Asn Ser Ser Ala
785                 790                 795                 800
Val Phe Leu Lys Trp Lys Ala Pro Glu Leu Lys Asp Arg His Gly Val
                805                 810                 815
Leu Leu Asn Tyr His Val Ile Val Arg Gly Ile Asp Thr Ala His Asn
            820                 825                 830
Phe Ser Arg Ile Leu Thr Asn Val Thr Ile Asp Ala Ala Ser Pro Thr
        835                 840                 845
Leu Val Leu Ala Asn Leu Thr Glu Gly Val Met Tyr Thr Val Gly Val
    850                 855                 860
Ala Ala Gly Asn Asn Ala Gly Val Gly Pro Tyr Cys Val Pro Ala Thr
865                 870                 875                 880
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Leu Arg Leu Asp Pro Ile Thr Lys Arg Leu Asp Pro Phe Ile Asn Gln
885 890 895
Arg Asp His Val Asn Asp Val Leu Thr Gln Pro Trp Phe Ile Ile Leu
900 905 910
Leu Gly Ala Ile Leu Ala Val Leu Met Leu Ser Phe Gly Ala Met Val
915 920 925
Phe Val Lys Arg Lys His Met Met Met Lys Gln Ser Ala Leu Asn Thr
930 935 940
Met Arg Gly Asn His Thr Ser Asp Val Leu Lys Met Pro Ser Leu Ser
945 950 955 960
Ala Arg Asn Gly Asn Gly Tyr Trp Leu Asp Ser Ser Thr Gly Gly Met
965 970 975
Val Trp Arg Pro Ser Pro Gly Gly Asp Ser Leu Glu Met Gln Lys Asp
980 985 990
His Ile Ala Asp Tyr Ala Pro Val Cys Gly Ala Pro Gly Ser Pro Ala
995 1000 1005
Gly Gly Gly Thr Ser Ser Gly Gly Ser Gly Gly Ala Gly Ser Gly Ala
1010 1015 1020
Ser Gly Gly Asp Asp Ile His Gly Gly His Gly Ser Glu Arg Asn Gln
1025 1030 1035 1040
Gln Arg Tyr Val Gly Glu Tyr Ser Asn Ile Pro Thr Asp Tyr Ala Glu
1045 1050 1055
Val Ser Ser Phe Gly Lys Ala Pro Ser Glu Tyr Gly Arg His Gly Asn
1060 1065 1070
Ala Ser Pro Ala Pro Tyr Ala Thr Ser Ser Ile Leu Ser Pro His Gln
1075 1080 1085
Gln Gln Gln Gln Gln Gln Pro Arg Tyr Gln Gln Arg Pro Val Pro Gly
1090 1095 1100
Tyr Gly Leu Gln Arg Pro Met His Pro His Tyr Gln Gln Gln Gln His
1105 1110 1115 1120
Gln Gln Gln Gln Ala Gln Gln Thr His Gln Gln His Gln Ala Leu Gln
1125 1130 1135
Gln His Gln Gln Leu Pro Pro Ser Asn Ile Tyr Gln Gln Met Ser Thr
1140 1145 1150
Thr Ser Glu Ile Tyr Pro Thr Asn Thr Gly Pro Ser Arg Ser Val Tyr
1155 1160 1165
Ser Glu Gln Tyr Tyr Tyr Pro Lys Asp Lys Gln Arg His Ile His Ile
1170 1175 1180

Thr Glu Asn Lys Leu Ser Asn Cys His Thr Tyr Glu Ala Ala Pro Gly
1185 1190 1195 1200
Ala Lys Gln Ser Ser Pro Ile Ser Ser Gln Phe Ala Ser Val Arg Arg
1205 1210 1215
Gln Gln Leu Pro Pro Asn Cys Ser Ile Gly Arg Glu Ser Ala Arg Phe
1220 1225 1230
Lys Val Leu Asn Thr Asp Gln Gly Lys Asn Gln Gln Asn Leu Leu Asp
1235 1240 1245
Leu Asp Gly Ser Ser Met Cys Tyr Asn Gly Leu Ala Asp Ser Gly Cys
1250 1255 1260
Gly Gly Ser Pro Ser Pro Met Ala Met Leu Met Ser His Glu Asp Glu
1265 1270 1275 1280
His Ala Leu Tyr His Thr Ala Asp Gly Asp Leu Asp Asp Met Glu Arg
1285 1290 1295
Leu Tyr Val Lys Val Asp Glu Gln Gln Pro Pro Gln Gln Gln Gln Gln
1300 1305 1310
Leu Ile Pro Leu Val Pro Gln His Pro Ala Glu Gly His Leu Gln Ser
1315 1320 1325
Trp Arg Asn Gln Ser Thr Arg Ser Ser Arg Lys Asn Gly Gln Glu Cys
1330 1335 1340
Ile Lys Glu Pro Ser Glu Leu Ile Tyr Ala Pro Gly Ser Val Ala Ser
1345 1350 1355 1360
Glu Arg Ser Leu Leu Ser Asn Ser Gly Ser Gly Thr Ser Ser Gln Pro
1365 1370 1375
Ala Gly His Asn Val
1380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3894 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGTACTATC TAGGTTTTTA CCACACTCAC ACACACACAC ACACATACAT AAATTTTGAT 60
AAAATTCCTA ATGCCTCAAA TCTCGCTCCC GTGATAATCG AACATCCCAT CGATGTGGTG 120
GTATCTAGGG GATCGCCAGC AACCCTCAAC TGTGGTGCAA AGCCATCTAC CGCCAAAATC 180

ACATGGTACA AGGATGGACA GCCCGTAATC ACGAATAAGG AGCAAGTGAA CAGCCACCGG 240

ATTGTTCTCG ACACGGGATC CCTGTTTCTT CTGAAAGTGA ATAGTGGAAA AAACGGAAAA 300

GACAGCGATG CGGGAGCGTA CTATTGTGTG GCCAGCAACG AGCACGGAGA AGTGAAGTCG 360

AACGAAGGAT CGTTAAAATT GGCGATGCTT CGCGAAGACT TTCGAGTTCG GCCAAGAACA 420

GTTCAGGCTC TTGGTGGAGA GATGGCCGTT CTGGAATGCA GTCCGCCACG TGGATTCCCG 480

GAGCCGGTTG TGAGCTGGCG GAAAGACGAC AAAGAGCTCC GAATTCAAGA CATGCCACGA 540

TACACTCTAC ACTCTGACGG AAACCTCATC ATTGATCCGG TCGATCGAAG CGATTCTGGT 600

ACTTATCAGT GTGTTGCCAA CAACATGGTC GGAGAACGGG TGTCCAATCC CGCAAGATTG 660

AGTGTCTTTG AGAAACCAAA GTTTGAGCAA GAACCCAAGG ACATGACGGT CGACGTCGGA 720

GCCGCAGTGC TGTTTGATTG TCGTGTGACT GGAGATCCTC AACCACAAAT TACGTGGAAA 780

CGCAAAAATG AGCCGATGCC AGTTACACGT GCATACATTG CCAAGGATAA TCGGGGGTTG 840

AGAATCGAAA GAGTTCAACC ATCAGACGAA GGTGAATACG TTTGCTATGC ACGAAATCCA 900

GCGGGAACTC TTGAAGCATC TGCACATCTT CGTGTCCAGG CACCTCCATC CTTCCAGACA 960

AAACCAGCAG ACCAGTCAGT TCCAGCTGGA GGCACGGCAA CTTTTGAATG CACCTTGGTC 1020

GGTCAACCGA GTCCCGCCTA TTTTTGGAGC AAGGAAGGCC AACAGGATCT TCTTTTCCCA 1080

AGTTATGTGT CCGCTGATGG TAGAACGAAA GTTTCACCAA CTGGAACATT GACAATTGAG 1140

GAAGTTCGTC AAGTTGATGA GGGAGCTTAT GTGTGCGCTG GAATGAACTC GGCAGGAAGC 1200

TCGTTGAGCA AGGCAGCTTT GAAAGCAACA TTTGAAACCA AAGGCCGTGT CCAAAAAAAA 1260

AAGAGCAAAA TGGGCAAACA GAAACAAAAA AATGTTCAAT CAATTATCAA ATATTTAATT 1320

TCAGCCGTGA CCGGAAACAC ACCCGCCAAA CCACCACCAA CAATCGAGCA TGGTCATCAA 1380

AATCAGACCC TTATGGTTGG ATCATCAGCC ATCCTTCCAT GTCAGGCTAG CGGAAAACCA 1440

ACTCCAGGAA TATCATGGCT CAGGGATGGG CTACCTATTG ACATTACAGA TAGTCGTATC 1500

AGTCAACATT CAACGGGAAG TCTACATATT GCCGATTTAA AGAAACCTGA CACCGGAGTT 1560

TACACTTGCA TTGCGAAGAA CGAGGATGGA GAGTCAACAT GGTCGGCATC TCTGACTGTT 1620

GAAGATCACA CTAGCAATGC ACAATTTGTT CGGATGCCGG ATCCATCGAA CTTCCCGTCT 1680

TCTCCAACGC AACCCATTAT TGTCAATGTC ACTGATACCG AAGTAGAGCT CCACTGGAAT 1740

GCTCCCTCCA CATCTGGCGC AGGACCAATC ACTGGTTATA TCATTCAGTA CTACAGTCCA 1800

GACCTCGGAC AGACGTGGTT TAACATTCCA GACTACGTGG CATCTACTGA ATATAGAATA 1860

AAGGGTCTGA AACCATCTCA CTCGTATATG TTTGTGATTC GAGCAGAAAA TGAGAAAGGT 1920

ATTGGAACGC CGAGTGTGTC GTCGGCTCTC GTTACCACTA GCAAGCCAGC AGCTCAAGTT 1980

GCGCTTTCTG ACAAGAACAA AATGGACATG GCCATCGCTG AGAAGAGACT CACTTCGGAA 2040

CAACTCATAA AACTCGAGGA AGTGAAGACT ATTAATTCTA CGGCCGTTCG TTTGTTCTGG 2100

AAGAAGAGGA AACTTGAAGA GCTGATTGAT GGTTACTACA TCAAGTGGAG AGGGCCTCCA 2160

AGAACCAATG ATAATCAATA CGTGAATGTG ACCAGCCCTA GCACCGAAAA CTATGTTGTT 2220

TCAAATTTAA TGCCATTCAC CAACTATGAG TTTTTCGTGA TTCCTTATCA TTCCGGAGTT 2280

CATAGTATTC ATGGAGCACC GAGTAATTCC ATGGACGTGT TGACCGCCGA AGCTCCACCT 2340

TCATTGCCAC CAGAGGATGT GCGAATCCGT ATGCTCAACC TGACCACTCT TCGTATCTCT 2400

TGGAAAGCAC CAAAAGCCGA CGGCATCAAC GGAATTCTCA AAGGATTCCA AATTGTTATT 2460

GTTGGTCAAG CGCCCAACAA CAATCGGAAC ATCACTACAA ACGAGAGAGC TGCCAGTGTT 2520
ACTCTGTTCC ATTTAGTGAC TGGAATGACG TATAAAATTC GTGTAGCGGC TAGAAGCAAT 2580
GGTGGAGTTG GAGTCTCACA TGGAACGAGT GAAGTCATCA TGAATCAAGA CACGCTGGAA 2640
AAACACCTTG CTGCTCAACA AGAAAACGAA TCATTTTTGT ATGGGCTGAT CAATAAATCT 2700
CATGTTCCTG TGATTGTCAT TGTTGCAATT CTGATTATTT TCGTAGTCAT CATTATAGCC 2760
TATTGTTACT GGAGGAATAG CAGAAACAGT GATGGAAAGG ATCGAAGTTT TATAAAGATC 2820
AATGATGGAA GTGTTCATAT GGCTTCGAAT AATCTTTGGG ATGTTGCACA AAATCCGAAT 2880
CAGAATCCAA TGTACAACAC TGCTGGAAGA ATGACTATGA ACAATAGAAA TGGCCAGGCT 2940
CTCTATTCGC TGACACCAAA TGCGCAAGAC TTTTTCAACA ATTGTGATGA CTACAGTGGA 3000
ACGATGCACA GACCAGGATC CGAGCATCAC TATCATTATG CTCAACTGAC TGGCGGACCT 3060
GGTAATGCGA TGTCTACTTT TTATGGAAAC CAATATCACG ATGATCCATC TCCATATGCC 3120
ACCACAACAC TGGTCCTGTC GAACCAACAA CCAGCTTGGC TCAATGACAA AATGCTTCGC 3180
GCGCCAGCAA TGCCAACAAA TCCCGTGCCA CCAGAGCCAC CGGCGCGATA TGCAGATCAT 3240
ACCGCTGGAA GACGATCTCG ATCGAGCCGT GCATCCGATG GGAGAGGAAC TCTGAATGGC 3300
GGACTCCATC ACCGGACTAG CGGAAGTCAA CGGTCGGATA GTCCACCTCA CACAGATGTG 3360
AGCTATGTTC AGCTTCACTC ATCCGATGGA ACTGGTAGTA GTAAGGAAAG AACTGGGGAG 3420
CGGAGAACAC CACCGAATAA GACTCTGATG GACTTTATTC CGCCACCACC TTCCAATCCA 3480
CCACCACCTG GAGGGCACGT TTATGACACA GCAACTAGGC GTCAGTTGAA TCGTGGAAGT 3540
ACTCCACGAG AAGACACCTA CGATTCGGTC AGTGACGGAG CTTTTGCTCG GGTTGATGTG 3600
AATGCAAGGC CAACGAGTCG GAATCGGAAT TTGGGAGGAA GGCCGCTGAA AGGGAAACGA 3660
GACGACGATA GTCAGCGGTC TTCGTTGATG ATGGACGATG ATGGTGGATC TTCTGAAGCT 3720
GACGGGGAGA ACTCTGAAGG AGACGTTCCG CGTGGAGGTG TTAGAAAAGC AGTTCCTCGA 3780
ATGGGTATCT CTGCAAGTAC GCTGGCTCAT AGTTGTTACG GGACAAACGG CACTGCTCAA 3840
CGATTCCGGT CAATTCCACG TAACAATGGA ATCGTCACAC AAGAACAAAC TTGA 3894

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Tyr Tyr Leu Gly Phe Tyr His Thr His Thr His Thr His Thr Tyr
1 5 10 15
Ile Asn Phe Asp Lys Ile Pro Asn Ala Ser Asn Leu Ala Pro Val Ile
20 25 30
Ile Glu His Pro Ile Asp Val Val Val Ser Arg Gly Ser Pro Ala Thr

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        35                  40                  45
Leu Asn Cys Gly Ala Lys Pro Ser Thr Ala Lys Ile Thr Trp Tyr Lys
    50                  55                  60
Asp Gly Gln Pro Val Ile Thr Asn Lys Glu Gln Val Asn Ser His Arg
65                  70                  75                  80
Ile Val Leu Asp Thr Gly Ser Leu Phe Leu Leu Lys Val Asn Ser Gly
                85                  90                  95
Lys Asn Gly Lys Asp Ser Asp Ala Gly Ala Tyr Tyr Cys Val Ala Ser
            100                 105                 110
Asn Glu His Gly Glu Val Lys Ser Asn Glu Gly Ser Leu Lys Leu Ala
        115                 120                 125
Met Leu Arg Glu Asp Phe Arg Val Arg Pro Arg Thr Val Gln Ala Leu
    130                 135                 140
Gly Gly Glu Met Ala Val Leu Glu Cys Ser Pro Pro Arg Gly Phe Pro
145                 150                 155                 160
Glu Pro Val Val Ser Trp Arg Lys Asp Asp Lys Glu Leu Arg Ile Gln
                165                 170                 175
Asp Met Pro Arg Tyr Thr Leu His Ser Asp Gly Asn Leu Ile Ile Asp
            180                 185                 190
Pro Val Asp Arg Ser Asp Ser Gly Thr Tyr Gln Cys Val Ala Asn Asn
        195                 200                 205
Met Val Gly Glu Arg Val Ser Asn Pro Ala Arg Leu Ser Val Phe Glu
    210                 215                 220
Lys Pro Lys Phe Glu Gln Glu Pro Lys Asp Met Thr Val Asp Val Gly
225                 230                 235                 240
Ala Ala Val Leu Phe Asp Cys Arg Val Thr Gly Asp Pro Gln Pro Gln
                245                 250                 255
Ile Thr Trp Lys Arg Lys Asn Glu Pro Met Pro Val Thr Arg Ala Tyr
            260                 265                 270
Ile Ala Lys Asp Asn Arg Gly Leu Arg Ile Glu Arg Val Gln Pro Ser
        275                 280                 285
Asp Glu Gly Glu Tyr Val Cys Tyr Ala Arg Asn Pro Ala Gly Thr Leu
    290                 295                 300
Glu Ala Ser Ala His Leu Arg Val Gln Ala Pro Pro Ser Phe Gln Thr
305                 310                 315                 320
Lys Pro Ala Asp Gln Ser Val Pro Ala Gly Gly Thr Ala Thr Phe Glu
                325                 330                 335
Cys Thr Leu Val Gly Gln Pro Ser Pro Ala Tyr Phe Trp Ser Lys Glu
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            340                 345                 350
Gly Gln Gln Asp Leu Leu Phe Pro Ser Tyr Val Ser Ala Asp Gly Arg
        355                 360                 365
Thr Lys Val Ser Pro Thr Gly Thr Leu Thr Ile Glu Glu Val Arg Gln
    370                 375                 380
Val Asp Glu Gly Ala Tyr Val Cys Ala Gly Met Asn Ser Ala Gly Ser
385                 390                 395                 400
Ser Leu Ser Lys Ala Ala Leu Lys Ala Thr Phe Glu Thr Lys Gly Arg
                405                 410                 415
Val Gln Lys Lys Lys Ser Lys Met Gly Lys Gln Lys Gln Lys Asn Val
            420                 425                 430
Gln Ser Ile Ile Lys Tyr Leu Ile Ser Ala Val Thr Gly Asn Thr Pro
        435                 440                 445
Ala Lys Pro Pro Pro Thr Ile Glu His Gly His Gln Asn Gln Thr Leu
    450                 455                 460
Met Val Gly Ser Ser Ala Ile Leu Pro Cys Gln Ala Ser Gly Lys Pro
465                 470                 475                 480
Thr Pro Gly Ile Ser Trp Leu Arg Asp Gly Leu Pro Ile Asp Ile Thr
                485                 490                 495
Asp Ser Arg Ile Ser Gln His Ser Thr Gly Ser Leu His Ile Ala Asp
            500                 505                 510
Leu Lys Lys Pro Asp Thr Gly Val Tyr Thr Cys Ile Ala Lys Asn Glu
        515                 520                 525
Asp Gly Glu Ser Thr Trp Ser Ala Ser Leu Thr Val Glu Asp His Thr
    530                 535                 540
Ser Asn Ala Gln Phe Val Arg Met Pro Asp Pro Ser Asn Phe Pro Ser
545                 550                 555                 560
Ser Pro Thr Gln Pro Ile Ile Val Asn Val Thr Asp Thr Glu Val Glu
                565                 570                 575
Leu His Trp Asn Ala Pro Ser Thr Ser Gly Ala Gly Pro Ile Thr Gly
            580                 585                 590
Tyr Ile Ile Gln Tyr Tyr Ser Pro Asp Leu Gly Gln Thr Trp Phe Asn
        595                 600                 605
Ile Pro Asp Tyr Val Ala Ser Thr Glu Tyr Arg Ile Lys Gly Leu Lys
    610                 615                 620
Pro Ser His Ser Tyr Met Phe Val Ile Arg Ala Glu Asn Glu Lys Gly
625                 630                 635                 640
Ile Gly Thr Pro Ser Val Ser Ser Ala Leu Val Thr Thr Ser Lys Pro
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645 650 655

Ala Ala Gln Val Ala Leu Ser Asp Lys Asn Lys Met Asp Met Ala Ile

660 665 670

Ala Glu Lys Arg Leu Thr Ser Glu Gln Leu Ile Lys Leu Glu Glu Val

675 680 685

Lys Thr Ile Asn Ser Thr Ala Val Arg Leu Phe Trp Lys Lys Arg Lys

690 695 700

Leu Glu Glu Leu Ile Asp Gly Tyr Tyr Ile Lys Trp Arg Gly Pro Pro

705 710 715 720

Arg Thr Asn Asp Asn Gln Tyr Val Asn Val Thr Ser Pro Ser Thr Glu

725 730 735

Asn Tyr Val Val Ser Asn Leu Met Pro Phe Thr Asn Tyr Glu Phe Phe

740 745 750

Val Ile Pro Tyr His Ser Gly Val His Ser Ile His Gly Ala Pro Ser

755 760 765

Asn Ser Met Asp Val Leu Thr Ala Glu Ala Pro Pro Ser Leu Pro Pro

770 775 780

Glu Asp Val Arg Ile Arg Met Leu Asn Leu Thr Thr Leu Arg Ile Ser

785 790 795 800

Trp Lys Ala Pro Lys Ala Asp Gly Ile Asn Gly Ile Leu Lys Gly Phe

805 810 815

Gln Ile Val Ile Val Gly Gln Ala Pro Asn Asn Asn Arg Asn Ile Thr

820 825 830

Thr Asn Glu Arg Ala Ala Ser Val Thr Leu Phe His Leu Val Thr Gly

835 840 845

Met Thr Tyr Lys Ile Arg Val Ala Ala Arg Ser Asn Gly Gly Val Gly

850 855 860

Val Ser His Gly Thr Ser Glu Val Ile Met Asn Gln Asp Thr Leu Glu

865 870 875 880

Lys His Leu Ala Ala Gln Gln Glu Asn Glu Ser Phe Leu Tyr Gly Leu

885 890 895

Ile Asn Lys Ser His Val Pro Val Ile Val Ile Val Ala Ile Leu Ile

900 905 910

Ile Phe Val Val Ile Ile Ile Ala Tyr Cys Tyr Trp Arg Asn Ser Arg

915 920 925

Asn Ser Asp Gly Lys Asp Arg Ser Phe Ile Lys Ile Asn Asp Gly Ser

930 935 940

Val His Met Ala Ser Asn Asn Leu Trp Asp Val Ala Gln Asn Pro Asn

945 950 955 960

Gln Asn Pro Met Tyr Asn Thr Ala Gly Arg Met Thr Met Asn Asn Arg

965 970 975

Asn Gly Gln Ala Leu Tyr Ser Leu Thr Pro Asn Ala Gln Asp Phe Phe

980 985 990

Asn Asn Cys Asp Asp Tyr Ser Gly Thr Met His Arg Pro Gly Ser Glu

995 1000 1005

His His Tyr His Tyr Ala Gln Leu Thr Gly Gly Pro Gly Asn Ala Met

1010 1015 1020

Ser Thr Phe Tyr Gly Asn Gln Tyr His Asp Asp Pro Ser Pro Tyr Ala

1025 1030 1035 1040

Thr Thr Thr Leu Val Leu Ser Asn Gln Gln Pro Ala Trp Leu Asn Asp

1045 1050 1055

Lys Met Leu Arg Ala Pro Ala Met Pro Thr Asn Pro Val Pro Pro Glu

1060 1065 1070

Pro Pro Ala Arg Tyr Ala Asp His Thr Ala Gly Arg Arg Ser Arg Ser

1075 1080 1085

Ser Arg Ala Ser Asp Gly Arg Gly Thr Leu Asn Gly Gly Leu His His

1090 1095 1100

Arg Thr Ser Gly Ser Gln Arg Ser Asp Ser Pro Pro His Thr Asp Val

1105 1110 1115 1120

Ser Tyr Val Gln Leu His Ser Ser Asp Gly Thr Gly Ser Ser Lys Glu

1125 1130 1135

Arg Thr Gly Glu Arg Arg Thr Pro Pro Asn Lys Thr Leu Met Asp Phe

1140 1145 1150

Ile Pro Pro Pro Pro Ser Asn Pro Pro Pro Pro Gly Gly His Val Tyr

1155 1160 1165

Asp Thr Ala Thr Arg Arg Gln Leu Asn Arg Gly Ser Thr Pro Arg Glu

1170 1175 1180

Asp Thr Tyr Asp Ser Val Ser Asp Gly Ala Phe Ala Arg Val Asp Val

1185 1190 1195 1200

Asn Ala Arg Pro Thr Ser Arg Asn Arg Asn Leu Gly Gly Arg Pro Leu

1205 1210 1215

Lys Gly Lys Arg Asp Asp Asp Ser Gln Arg Ser Ser Leu Met Met Asp

1220 1225 1230

Asp Asp Gly Gly Ser Ser Glu Ala Asp Gly Glu Asn Ser Glu Gly Asp

1235 1240 1245

Val Pro Arg Gly Gly Val Arg Lys Ala Val Pro Arg Met Gly Ile Ser

1250 1255 1260

Ala Ser Thr Leu Ala His Ser Cys Tyr Gly Thr Asn Gly Thr Ala Gln

1265 1270 1275 1280

Arg Phe Arg Ser Ile Pro Arg Asn Asn Gly Ile Val Thr Gln Glu Gln

1285 1290 1295

Thr

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4956 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAAATGGA AACATGTTCC TTTTTTGGTC ATGATATCAC TCCTCAGCTT ATCCCCAAAT 60

CACCTGTTTC TGGCCCAGCT TATTCCAGAC CCTGAAGATG TAGAGAGGGG GAACGACCAC 120

GGGACGCCAA TCCCCACCTC TGATAACGAT GACAATTCGC TGGGCTATAC AGGCTCCCGT 180

CTTCGTCAGG AAGATTTTCC ACCTCGCATT GTTGAACACC CTTCAGACCT GATTGTCTCA 240

AAAGGAGAAC CTGCAACTTT GAACTGCAAA GCTGAAGGCC GCCCCACACC CACTATTGAA 300

TGGTACAAAG GGGGAGAGAG AGTGGAGACA GACAAAGATG ACCCTCGCTC ACACCGAATG 360

TTGCTGCCGA GTGGATCTTT ATTTTTCTTA CGTATAGTAC ATGGACGGAA AAGTAGACCT 420

GATGAAGGAG TCTATGTCTG TGTAGCAAGG AATTACCTTG GAGAGGCTGT GAGCCACAAT 480

GCATCGCTGG AAGTAGCCAT ACTTCGGGAT GACTTCAGAC AAAACCCTTC GGATGTCATG 540

GTTGCAGTAG GAGAGCCTGC AGTAATGGAA TGCCAACCTC CACGAGGCCA TCCTGAGCCC 600

ACCATTTCAT GGAAGAAAGA TGGCTCTCCA CTGGATGATA AAGATGAAAG AATAACTATA 660

CGAGGAGGAA AGCTCATGAT CACTTACACC CGTAAAAGTG ACGCTGGCAA ATATGTTTGT 720

GTTGGTACCA ATATGGTTGG GGAACGTGAG AGTGAAGTAG CCGAGCTGAC TGTCTTAGAG 780

AGACCATCAT TTGTGAAGAG ACCCAGTAAC TTGGCAGTAA CTGTGGATGA CAGTGCAGAA 840

TTTAAATGTG AGGCCCGAGG TGACCCTGTA CCTACAGTAC GATGGAGGAA AGATGATGGA 900

GAGCTGCCCA AATCCAGATA TGAAATCCGA GATGATCATA CCTTGAAAAT TAGGAAGGTG 960

ACAGCTGGTG ACATGGGTTC ATACACTTGT GTTGCAGAAA ATATGGTGGG CAAAGCTGAA 1020

GCATCTGCTA CTCTGACTGT TCAAGAACCT CCACATTTTG TTGTGAAACC CCGTGACCAG 1080

GTTGTTGCTT TGGGACGGAC TGTAACTTTT CAGTGTGAAG CAACCGGAAA TCCTCAACCA 1140

GCTATTTTCT GGAGGAGAGA AGGGAGTCAG AATCTACTTT TCTCATATCA ACCACCACAG 1200

TCATCCAGCC GATTTTCAGT CTCCCAGACT GGCGACCTCA CAATTACTAA TGTCCAGCGA 1260

TCTGATGTTG GTTATTACAT CTGCCAGACT TTAAATGTTG CTGGAAGCAT CATCACAAAG 1320

GCATATTTGG AAGTTACAGA TGTGATTGCA GATCGGCCTC CCCCAGTTAT TCGACAAGGT 1380

CCTGTGAATC AGACTGTAGC CGTGGATGGC ACTTTCGTCC TCAGCTGTGT GGCCACAGGC 1440

AGTCCAGTGC CCACCATTCT GTGGAGAAAG GATGGAGTCC TCGTTTCAAC CCAAGACTCT 1500

CGAATCAAAC AGTTGGAGAA TGGAGTACTG CAGATCCGAT ATGCTAAGCT GGGTGATACT 1560

GGTCGGTACA CCTGCATTGC ATCAACCCCC AGTGGTGAAG CAACATGGAG TGCTTACATT 1620

GAAGTTCAAG AATTTGGAGT TCCAGTTCAG CCTCCAAGAC CTACTGACCC AAATTTAATC 1680

CCTAGTGCCC CATCAAAACC TGAAGTGACA GATGTCAGCA GAAATACAGT CACATTATCG 1740

TGGCAACCAA ATTTGAATTC AGGAGCAACT CCAACATCTT ATATTATAGA AGCCTTCAGC 1800

CATGCATCTG GTAGCAGCTG GCAGACCGTA GCAGAGAATG TGAAAACAGA AACATCTGCC 1860

ATTAAAGGAC TCAAACCTAA TGCAATTTAC CTTTTCCTTG TGAGGGCAGC TAATGCATAT 1920

GGAATTAGTG ATCCAAGCCA AATATCAGAT CCAGTGAAAA CACAAGATGT CCTACCAACA 1980

AGTCAGGGGG TGGACCACAA GCAGGTCCAG AGAGAGCTGG GAAATGCTGT TCTGCACCTC 2040

CACAACCCCA CCGTCCTTTC TTCCTCTTCC ATCGAAGTGC ACTGGACAGT AGATCAACAG 2100

TCTCAGTATA TACAAGGATA TAAAATTCTC TATCGGCCAT CTGGAGCCAA CCACGGAGAA 2160

TCAGACTGGT TAGTTTTTGA AGTGAGGACG CCAGCCAAAA ACAGTGTGGT AATCCCTGAT 2220

CTCAGAAAGG GAGTCAACTA TGAAATTAAG GCTCGCCCTT TTTTTAATGA ATTTCAAGGA 2280

GCAGATAGTG AAATCAAGTT TGCCAAAACC CTGGAAGAAG CACCCAGTGC CCCACCCCAA 2340

GGTGTAACTG TATCCAAGAA TGATGGAAAC GGAACTGCAA TTCTAGTTAG TTGGCAGCCA 2400

CCTCCAGAAG ACACTCAAAA TGGAATGGTC CAAGAGTATA AGGTTTGGTG TCTGGGCAAT 2460

GAAACTCGAT ACCACATCAA CAAAACAGTG GATGGTTCCA CCTTTTCCGT GGTCATTCCC 2520

TTTCTTGTTC CTGGAATCCG ATACAGTGTG GAAGTGGCAG CCAGCACTGG GGCTGGGTCT 2580

GGGGTAAAGA GTGAGCCTCA GTTCATCCAG CTGGATGCCC ATGGAAACCC TGTGTCACCT 2640

GAGGACCAAG TCAGCCTCGC TCAGCAGATT TCAGATGTGG TGAAGCAGCC GGCCTTCATA 2700

GCAGGTATTG GAGCAGCCTG TTGGATCATC CTCATGGTCT TCAGCATCTG GCTTTATCGA 2760

CACCGCAAGA AGAGAAACGG ACTTACTAGT ACCTACGCGG GTATCAGAAA AGTCCCGTCT 2820

TTTACCTTCA CACCAACAGT AACTTACCAG AGAGGAGGCG AAGCTGTCAG CAGTGGAGGG 2880

AGGCCTGGAC TTCTCAACAT CAGTGAACCT GCCGCGCAGC CATGGCTGGC AGACACGTGG 2940

CCTAATACTG GCAACAACCA CAATGACTGC TCCATCAGCT GCTGCACGGC AGGCAATGGA 3000

AACAGCGACA GCAACCTCAC TACCTACAGT CGCCCAGCTG ATTGTATAGC AAATTATAAC 3060

AACCAACTGG ATAACAAACA AACAAATCTG ATGCTCCCTG AGTCAACTGT TTATGGTGAT 3120

GTGGACCTTA GTAACAAAAT CAATGAGATG AAAACCTTCA ATAGCCCAAA TCTGAAGGAT 3180

GGGCGTTTTG TCAATCCATC AGGGCAGCCT ACTCCTTACG CCACCACTCA GCTCATCCAG 3240

TCAAACCTCA GCAACAACAT GAACAATGGC AGCGGGGACT CTGGCGAGAA GCACTGGAAA 3300

CCACTGGGAC AGCAGAAACA AGAAGTGGCA CCAGTTCAGT ACAACATCGT GGAGCAAAAC 3360

AAGCTGAACA AAGATTATCG AGCAAATGAC ACAGTTCCTC CAACTATCCC ATACAACCAA 3420

TCATACGACC AGAACACAGG AGGATCCTAC AACAGCTCAG ACCGGGGCAG TAGTACATCT 3480

GGGAGTCAGG GGCACAAGAA AGGGGCAAGA ACACCCAAGG TACCAAAACA GGGTGGCATG 3540

AACTGGGCAG ACCTGCTTCC TCCTCCCCCA GCACATCCTC CTCCACACAG CAATAGCGAA 3600

GAGTACAACA TTTCTGTAGA TGAAAGCTAT GACCAAGAAA TGCCATGTCC CGTGCCACCA 3660

GCAAGGATGT ATTTGCAACA AGATGAATTA GAAGAGGAGG AAGATGAACG AGGCCCCACT 3720
CCCCCTGTTC GGGGAGCAGC TTCTTCTCCA GCTGCCGTGT CCTATAGCCA TCAGTCCACT 3780
GCCACTCTGA CTCCCTCCCC ACAGGAAGAA CTCCAGCCCA TGTTACAGGA TTGTCCAGAG 3840
GAGACTGGCC ACATGCAGCA CCAGCCCGAC AGGAGACGGC AGCCTGTGAG TCCTCCTCCA 3900
CCACCACGGC CGATCTCCCC TCCACATACC TATGGCTACA TTTCAGGACC CCTGGTCTCA 3960
GATATGGATA CGGATGCGCC AGAAGAGGAA GAAGACGAAG CCGACATGGA GGTAGCCAAG 4020
ATGCAAACCA GAAGGCTTTT GTTACGTGGG CTTGAGCAGA CACCTGCCTC CAGTGTTGGG 4080
GACCTGGAGA GCTCTGTCAC GGGGTCCATG ATCAACGGCT GGGGCTCAGC CTCAGAGGAG 4140
GACAACATTT CCAGCGGACG CTCCAGTGTT AGTTCTTCGG ACGGCTCCTT TTTCACTGAT 4200
GCTGACTTTG CCCAGGCAGT CGCAGCAGCG GCAGAGTATG CTGGTCTGAA AGTAGCACGA 4260
CGGCAAATGC AGGATGCTGC TGGCCGTCGA CATTTTCATG CGTCTCAGTG CCCTAGGCCC 4320
ACAAGTCCCG TGTCTACAGA CAGCAACATG AGTGCCGCCG TAATGCAGAA AACCAGACCA 4380
GCCAAGAAAC TGAAACACCA GCCAGGACAT CTGCGCAGAG AAACCTACAC AGATGATCTT 4440
CCACCACCTC CTGTGCCGCC ACCTGCTATA AAGTCACCTA CTGCCCAATC CAAGACACAG 4500
CTGGAAGTAC GACCTGTAGT GGTGCCAAAA CTCCCTTCTA TGGATGCAAG AACAGACAGA 4560
TCATCAGACA GAAAAGGAAG CAGTTACAAG GGGAGAGAAG TGTTGGATGG AAGACAGGTT 4620
GTTGACATGC GAACAAATCC AGGTGATCCC AGAGAAGCAC AGGAACAGCA AAATGACGGG 4680
AAAGGACGTG GAAACAAGGC AGCAAAACGA GACCTTCCAC CAGCAAAGAC TCATCTCATC 4740
CAAGAGGATA TTCTACCTTA TTGTAGACCT ACTTTTCCAA CATCAAATAA TCCCAGAGAT 4800
CCCAGTTCCT CAAGCTCAAT GTCATCAAGA GGATCAGGAA GCAGACAAAG AGAACAAGCA 4860
AATGTAGGTC GAAGAAATAT TGCAGAAATG CAGGTACTTG GAGGATATGA AAGAGGAGAA 4920
GATAATAATG AAGAATTAGA GGAAACTGAA AGCTGA 4956

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1651 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Lys Trp Lys His Val Pro Phe Leu Val Met Ile Ser Leu Leu Ser
1 5 10 15
Leu Ser Pro Asn His Leu Phe Leu Ala Gln Leu Ile Pro Asp Pro Glu
20 25 30
Asp Val Glu Arg Gly Asn Asp His Gly Thr Pro Ile Pro Thr Ser Asp
35 40 45
Asn Asp Asp Asn Ser Leu Gly Tyr Thr Gly Ser Arg Leu Arg Gln Glu

50 55 60

Asp Phe Pro Pro Arg Ile Val Glu His Pro Ser Asp Leu Ile Val Ser

65 70 75 80

Lys Gly Glu Pro Ala Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr

85 90 95

Pro Thr Ile Glu Trp Tyr Lys Gly Gly Glu Arg Val Glu Thr Asp Lys

100 105 110

Asp Asp Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe

115 120 125

Phe Leu Arg Ile Val His Gly Arg Lys Ser Arg Pro Asp Glu Gly Val

130 135 140

Tyr Val Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser His Asn

145 150 155 160

Ala Ser Leu Glu Val Ala Ile Leu Arg Asp Asp Phe Arg Gln Asn Pro

165 170 175

Ser Asp Val Met Val Ala Val Gly Glu Pro Ala Val Met Glu Cys Gln

180 185 190

Pro Pro Arg Gly His Pro Glu Pro Thr Ile Ser Trp Lys Lys Asp Gly

195 200 205

Ser Pro Leu Asp Asp Lys Asp Glu Arg Ile Thr Ile Arg Gly Gly Lys

210 215 220

Leu Met Ile Thr Tyr Thr Arg Lys Ser Asp Ala Gly Lys Tyr Val Cys

225 230 235 240

Val Gly Thr Asn Met Val Gly Glu Arg Glu Ser Glu Val Ala Glu Leu

245 250 255

Thr Val Leu Glu Arg Pro Ser Phe Val Lys Arg Pro Ser Asn Leu Ala

260 265 270

Val Thr Val Asp Asp Ser Ala Glu Phe Lys Cys Glu Ala Arg Gly Asp

275 280 285

Pro Val Pro Thr Val Arg Trp Arg Lys Asp Asp Gly Glu Leu Pro Lys

290 295 300

Ser Arg Tyr Glu Ile Arg Asp Asp His Thr Leu Lys Ile Arg Lys Val

305 310 315 320

Thr Ala Gly Asp Met Gly Ser Tyr Thr Cys Val Ala Glu Asn Met Val

325 330 335

Gly Lys Ala Glu Ala Ser Ala Thr Leu Thr Val Gln Glu Pro Pro His

340 345 350

Phe Val Val Lys Pro Arg Asp Gln Val Val Ala Leu Gly Arg Thr Val

```
        355                 360                 365
Thr Phe Gln Cys Glu Ala Thr Gly Asn Pro Gln Pro Ala Ile Phe Trp
    370                 375                 380
Arg Arg Glu Gly Ser Gln Asn Leu Leu Phe Ser Tyr Gln Pro Pro Gln
385                 390                 395                 400
Ser Ser Ser Arg Phe Ser Val Ser Gln Thr Gly Asp Leu Thr Ile Thr
                405                 410                 415
Asn Val Gln Arg Ser Asp Val Gly Tyr Tyr Ile Cys Gln Thr Leu Asn
            420                 425                 430
Val Ala Gly Ser Ile Ile Thr Lys Ala Tyr Leu Glu Val Thr Asp Val
        435                 440                 445
Ile Ala Asp Arg Pro Pro Pro Val Ile Arg Gln Gly Pro Val Asn Gln
    450                 455                 460
Thr Val Ala Val Asp Gly Thr Phe Val Leu Ser Cys Val Ala Thr Gly
465                 470                 475                 480
Ser Pro Val Pro Thr Ile Leu Trp Arg Lys Asp Gly Val Leu Val Ser
                485                 490                 495
Thr Gln Asp Ser Arg Ile Lys Gln Leu Glu Asn Gly Val Leu Gln Ile
            500                 505                 510
Arg Tyr Ala Lys Leu Gly Asp Thr Gly Arg Tyr Thr Cys Ile Ala Ser
        515                 520                 525
Thr Pro Ser Gly Glu Ala Thr Trp Ser Ala Tyr Ile Glu Val Gln Glu
    530                 535                 540
Phe Gly Val Pro Val Gln Pro Pro Arg Pro Thr Asp Pro Asn Leu Ile
545                 550                 555                 560
Pro Ser Ala Pro Ser Lys Pro Glu Val Thr Asp Val Ser Arg Asn Thr
                565                 570                 575
Val Thr Leu Ser Trp Gln Pro Asn Leu Asn Ser Gly Ala Thr Pro Thr
            580                 585                 590
Ser Tyr Ile Ile Glu Ala Phe Ser His Ala Ser Gly Ser Ser Trp Gln
        595                 600                 605
Thr Val Ala Glu Asn Val Lys Thr Glu Thr Ser Ala Ile Lys Gly Leu
    610                 615                 620
Lys Pro Asn Ala Ile Tyr Leu Phe Leu Val Arg Ala Ala Asn Ala Tyr
625                 630                 635                 640
Gly Ile Ser Asp Pro Ser Gln Ile Ser Asp Pro Val Lys Thr Gln Asp
                645                 650                 655
Val Leu Pro Thr Ser Gln Gly Val Asp His Lys Gln Val Gln Arg Glu
```

660 665 670

Leu Gly Asn Ala Val Leu His Leu His Asn Pro Thr Val Leu Ser Ser

675 680 685

Ser Ser Ile Glu Val His Trp Thr Val Asp Gln Gln Ser Gln Tyr Ile

690 695 700

Gln Gly Tyr Lys Ile Leu Tyr Arg Pro Ser Gly Ala Asn His Gly Glu

705 710 715 720

Ser Asp Trp Leu Val Phe Glu Val Arg Thr Pro Ala Lys Asn Ser Val

725 730 735

Val Ile Pro Asp Leu Arg Lys Gly Val Asn Tyr Glu Ile Lys Ala Arg

740 745 750

Pro Phe Phe Asn Glu Phe Gln Gly Ala Asp Ser Glu Ile Lys Phe Ala

755 760 765

Lys Thr Leu Glu Glu Ala Pro Ser Ala Pro Pro Gln Gly Val Thr Val

770 775 780

Ser Lys Asn Asp Gly Asn Gly Thr Ala Ile Leu Val Ser Trp Gln Pro

785 790 795 800

Pro Pro Glu Asp Thr Gln Asn Gly Met Val Gln Glu Tyr Lys Val Trp

805 810 815

Cys Leu Gly Asn Glu Thr Arg Tyr His Ile Asn Lys Thr Val Asp Gly

820 825 830

Ser Thr Phe Ser Val Val Ile Pro Phe Leu Val Pro Gly Ile Arg Tyr

835 840 845

Ser Val Glu Val Ala Ala Ser Thr Gly Ala Gly Ser Gly Val Lys Ser

850 855 860

Glu Pro Gln Phe Ile Gln Leu Asp Ala His Gly Asn Pro Val Ser Pro

865 870 875 880

Glu Asp Gln Val Ser Leu Ala Gln Gln Ile Ser Asp Val Val Lys Gln

885 890 895

Pro Ala Phe Ile Ala Gly Ile Gly Ala Ala Cys Trp Ile Ile Leu Met

900 905 910

Val Phe Ser Ile Trp Leu Tyr Arg His Arg Lys Lys Arg Asn Gly Leu

915 920 925

Thr Ser Thr Tyr Ala Gly Ile Arg Lys Val Pro Ser Phe Thr Phe Thr

930 935 940

Pro Thr Val Thr Tyr Gln Arg Gly Gly Glu Ala Val Ser Ser Gly Gly

945 950 955 960

Arg Pro Gly Leu Leu Asn Ile Ser Glu Pro Ala Ala Gln Pro Trp Leu

965 970 975

Ala Asp Thr Trp Pro Asn Thr Gly Asn Asn His Asn Asp Cys Ser Ile

980 985 990

Ser Cys Cys Thr Ala Gly Asn Gly Asn Ser Asp Ser Asn Leu Thr Thr

995 1000 1005

Tyr Ser Arg Pro Ala Asp Cys Ile Ala Asn Tyr Asn Asn Gln Leu Asp

1010 1015 1020

Asn Lys Gln Thr Asn Leu Met Leu Pro Glu Ser Thr Val Tyr Gly Asp

1025 1030 1035 1040

Val Asp Leu Ser Asn Lys Ile Asn Glu Met Lys Thr Phe Asn Ser Pro

1045 1050 1055

Asn Leu Lys Asp Gly Arg Phe Val Asn Pro Ser Gly Gln Pro Thr Pro

1060 1065 1070

Tyr Ala Thr Thr Gln Leu Ile Gln Ser Asn Leu Ser Asn Asn Met Asn

1075 1080 1085

Asn Gly Ser Gly Asp Ser Gly Glu Lys His Trp Lys Pro Leu Gly Gln

1090 1095 1100

Gln Lys Gln Glu Val Ala Pro Val Gln Tyr Asn Ile Val Glu Gln Asn

1105 1110 1115 1120

Lys Leu Asn Lys Asp Tyr Arg Ala Asn Asp Thr Val Pro Pro Thr Ile

1125 1130 1135

Pro Tyr Asn Gln Ser Tyr Asp Gln Asn Thr Gly Gly Ser Tyr Asn Ser

1140 1145 1150

Ser Asp Arg Gly Ser Ser Thr Ser Gly Ser Gln Gly His Lys Lys Gly

1155 1160 1165

Ala Arg Thr Pro Lys Val Pro Lys Gln Gly Gly Met Asn Trp Ala Asp

1170 1175 1180

Leu Leu Pro Pro Pro Pro Ala His Pro Pro Pro His Ser Asn Ser Glu

1185 1190 1195 1200

Glu Tyr Asn Ile Ser Val Asp Glu Ser Tyr Asp Gln Glu Met Pro Cys

1205 1210 1215

Pro Val Pro Pro Ala Arg Met Tyr Leu Gln Gln Asp Glu Leu Glu Glu

1220 1225 1230

Glu Glu Asp Glu Arg Gly Pro Thr Pro Pro Val Arg Gly Ala Ala Ser

1235 1240 1245

Ser Pro Ala Ala Val Ser Tyr Ser His Gln Ser Thr Ala Thr Leu Thr

1250 1255 1260

Pro Ser Pro Gln Glu Glu Leu Gln Pro Met Leu Gln Asp Cys Pro Glu

1265 1270 1275 1280

Glu Thr Gly His Met Gln His Gln Pro Asp Arg Arg Arg Gln Pro Val

1285 1290 1295

Ser Pro Pro Pro Pro Pro Arg Pro Ile Ser Pro Pro His Thr Tyr Gly

1300 1305 1310

Tyr Ile Ser Gly Pro Leu Val Ser Asp Met Asp Thr Asp Ala Pro Glu

1315 1320 1325

Glu Glu Glu Asp Glu Ala Asp Met Glu Val Ala Lys Met Gln Thr Arg

1330 1335 1340

Arg Leu Leu Leu Arg Gly Leu Glu Gln Thr Pro Ala Ser Ser Val Gly

1345 1350 1355 1360

Asp Leu Glu Ser Ser Val Thr Gly Ser Met Ile Asn Gly Trp Gly Ser

1365 1370 1375

Ala Ser Glu Glu Asp Asn Ile Ser Ser Gly Arg Ser Ser Val Ser Ser

1380 1385 1390

Ser Asp Gly Ser Phe Phe Thr Asp Ala Asp Phe Ala Gln Ala Val Ala

1395 1400 1405

Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln Met Gln

1410 1415 1420

Asp Ala Ala Gly Arg Arg His Phe His Ala Ser Gln Cys Pro Arg Pro

1425 1430 1435 1440

Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser Ala Ala Val Met Gln

1445 1450 1455

Lys Thr Arg Pro Ala Lys Lys Leu Lys His Gln Pro Gly His Leu Arg

1460 1465 1470

Arg Glu Thr Tyr Thr Asp Asp Leu Pro Pro Pro Pro Val Pro Pro Pro

1475 1480 1485

Ala Ile Lys Ser Pro Thr Ala Gln Ser Lys Thr Gln Leu Glu Val Arg

1490 1495 1500

Pro Val Val Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr Asp Arg

1505 1510 1515 1520

Ser Ser Asp Arg Lys Gly Ser Ser Tyr Lys Gly Arg Glu Val Leu Asp

1525 1530 1535

Gly Arg Gln Val Val Asp Met Arg Thr Asn Pro Gly Asp Pro Arg Glu

1540 1545 1550

Ala Gln Glu Gln Gln Asn Asp Gly Lys Gly Arg Gly Asn Lys Ala Ala

1555 1560 1565

Lys Arg Asp Leu Pro Pro Ala Lys Thr His Leu Ile Gln Glu Asp Ile

1570 1575 1580

Leu Pro Tyr Cys Arg Pro Thr Phe Pro Thr Ser Asn Asn Pro Arg Asp

1585 1590 1595 1600

Pro Ser Ser Ser Ser Ser Met Ser Ser Arg Gly Ser Gly Ser Arg Gln

1605 1610 1615

Arg Glu Gln Ala Asn Val Gly Arg Arg Asn Ile Ala Glu Met Gln Val

1620 1625 1630

Leu Gly Gly Tyr Glu Arg Gly Glu Asp Asn Asn Glu Glu Leu Glu Glu

1635 1640 1645

Thr Glu Ser

1650

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 855..1187

(D) OTHER INFORMATION: /note= "N signifies gap in sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGATTGTTG CTCAAGGTCG AACAGTGACA TTTCCCTGTG AAACTAAAGG AAACCCACAG 60

CCAGCTGTTT TTTGGCAGAA AGAAGGCAGC CAGAACCTAC TTTTCCCAAA CCAACCCCAG 120

CAGCCCAACA GTAGATGCTC AGTGTCACCA ACTGGAGACC TCACAATCAC CAACATTCAA 180

CGTTCCGACG CGGGTTACTA CATCTGCCAG GCTTTAACTG TGGCAGGAAG CATTTTAGCA 240

AAAGCTCAAC TGGAGGTTAC TGATGTTTTG ACAGATAGAC CTCCACCTAT AATTCTACAA 300

GGCCCAGCCA ACCAAACGCT GGCAGTGGAT GGTACAGCGT TACTGAAATG TAAAGCCACT 360

GGTGATCCTC TTCCTGTAAT TAGCTGGTTA AAGGAGGGAT TTACTTTTCC GGGTAGAGAT 420

CCAAGAGCAA CAATTCAAGA GCAAGGCACA CTGCAGATTA AGAATTTACG GATTTCTGAT 480

ACTGGCACTT ATACTTGTGT GGCTACAAGT TCAAGTGGAG AGGCTTCCTG GAGTGCAGTG 540

CTGGATGTGA CAGAGTCTGG AGCAACAATC AGTAAAAACT ATGATTTAAG TGACCTGCCA 600

GGGCCACCAT CCAAACCGCA AGTCACTGAT GTTACTAAGA ACAGTGTCAC CTTGTCCTGG 660

CAGCCAGGTA CCCCTGGAAC CCTTCCAGCA AGTGCATATA TCATTGAGGC TTTCAGCCAA 720

TCAGTGAGCA ACAGCTGGCA GACCGTGGCA AACCATGTAA AGACCACCCT CTATACTGTA 780

AGAGGACTGC GGCCCAATAC AATCTACTTA TTCATGGTCA GAGCGATCAA CCCCAAGGTY 840

TCAGTGACCC AAGTNAAACC ACAGAAAAAC AATGGATCCA CTTGGGCCAA TGTCCCTCTA 900

CCTCCCCCCC CAGTCCAGCC CCTTCCTGGC ACGGAGCTGG AACACTATGC AGTGGAACAA 960

CAAGAAAATG GCTATGACAG TGATAGCTGG TGCCCACCAT TGCCAGTACA AACTTACTTA 1020

CACCAAGGTC TGGAAGATGA ACTGGAAGAA GATGATGATA GGGTCCCAAC ACCTCCTGTT 1080

CGAGGCGTGG CTTCTTCTCC TGCTATCTCC TTTGGACAGC AGTCCACTGC AACTCTTACT 1140

CCATCCCCAC GGGAAGAGAT GCAACCCATG CTGCAGGCTT CACCTNTTTA CCTCCTCTCA 1200

AAGACCTCGA CCTACCAGCC CATTTTCTAC TGACAGTAAC ACCAGTGCAG CCCTGAGTCA 1260

AAGTCAGAGG CCTCGGCCCA CTAAAAAACA CAAGGGAGGG 1300

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 434 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 285..396

(D) OTHER INFORMATION: /note= "Xaa signifies gap in sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Ile Val Ala Gln Gly Arg Thr Val Thr Phe Pro Cys Glu Thr Lys
1 5 10 15

Gly Asn Pro Gln Pro Ala Val Phe Trp Gln Lys Glu Gly Ser Gln Asn
20 25 30

Leu Leu Phe Pro Asn Gln Pro Gln Gln Pro Asn Ser Arg Cys Ser Val
35 40 45

Ser Pro Thr Gly Asp Leu Thr Ile Thr Asn Ile Gln Arg Ser Asp Ala
50 55 60

Gly Tyr Tyr Ile Cys Gln Ala Leu Thr Val Ala Gly Ser Ile Leu Ala
65 70 75 80

Lys Ala Gln Leu Glu Val Thr Asp Val Leu Thr Asp Arg Pro Pro Pro
85 90 95

Ile Ile Leu Gln Gly Pro Ala Asn Gln Thr Leu Ala Val Asp Gly Thr
100 105 110

Ala Leu Leu Lys Cys Lys Ala Thr Gly Asp Pro Leu Pro Val Ile Ser
115 120 125

Trp Leu Lys Glu Gly Phe Thr Phe Pro Gly Arg Asp Pro Arg Ala Thr

130 135 140

Ile Gln Glu Gln Gly Thr Leu Gln Ile Lys Asn Leu Arg Ile Ser Asp
145 150 155 160

Thr Gly Thr Tyr Thr Cys Val Ala Thr Ser Ser Ser Gly Glu Ala Ser
165 170 175

Trp Ser Ala Val Leu Asp Val Thr Glu Ser Gly Ala Thr Ile Ser Lys
180 185 190

Asn Tyr Asp Leu Ser Asp Leu Pro Gly Pro Pro Ser Lys Pro Gln Val
195 200 205

Thr Asp Val Thr Lys Asn Ser Val Thr Leu Ser Trp Gln Pro Gly Thr
210 215 220

Pro Gly Thr Leu Pro Ala Ser Ala Tyr Ile Ile Glu Ala Phe Ser Gln
225 230 235 240

Ser Val Ser Asn Ser Trp Gln Thr Val Ala Asn His Val Lys Thr Thr
245 250 255

Leu Tyr Thr Val Arg Gly Leu Arg Pro Asn Thr Ile Tyr Leu Phe Met
260 265 270

Val Arg Ala Ile Asn Pro Lys Val Ser Val Thr Gln Xaa Lys Pro Gln
275 280 285

Lys Asn Asn Gly Ser Thr Trp Ala Asn Val Pro Leu Pro Pro Pro Pro
290 295 300

Val Gln Pro Leu Pro Gly Thr Glu Leu Glu His Tyr Ala Val Glu Gln
305 310 315 320

Gln Glu Asn Gly Tyr Asp Ser Asp Ser Trp Cys Pro Pro Leu Pro Val
325 330 335

Gln Thr Tyr Leu His Gln Gly Leu Glu Asp Glu Leu Glu Glu Asp Asp
340 345 350

Asp Arg Val Pro Thr Pro Pro Val Arg Gly Val Ala Ser Ser Pro Ala
355 360 365

Ile Ser Phe Gly Gln Gln Ser Thr Ala Thr Leu Thr Pro Ser Pro Arg
370 375 380

Glu Glu Met Gln Pro Met Leu Gln Ala Ser Pro Xaa Phe Thr Ser Ser
385 390 395 400

Gln Arg Pro Arg Pro Thr Ser Pro Phe Ser Thr Asp Ser Asn Thr Ser
405 410 415

Ala Ala Leu Ser Gln Ser Gln Arg Pro Arg Pro Thr Lys Lys His Lys
420 425 430

Gly Gly

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 444 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
GCCCAGGCAG TTGCTGCAGC TGCGGAGTAT GCGGGCCTGA AAGTGGCTCG CCGCCAAATG      60
CAAGATGCTG CTGGCCGCCG CCACTTCCAT GCCTCTCAGT GCCCAAGGCC CACGAGTCCT     120
GTGTCCACAG ACAGCAACAT GAGTGCTGTT GTGATCCAGA AAGCCAGACC CGCCAAGAAG     180
CAGAAACACC AGCCAGGACA TCTGCGCAGG GAAGCCTACG CAGATGATCT TCCACCCCCT     240
CCAGTGCCAC CACCTGCTAT AAAATCGCCC ACTGTCCAGT CCAAGGCACA GCTGGAGGTA     300
CGGCCTGTCA TGGTGCCAAA ACTCGCGTCT ATAGAAGCAA GGACAGATAG ATCGTCAGAC     360
AGAAAAGGAG GCAGTTACAA GGGGAGAGAA GCTCTGGATG GAAGACAAGT CACTGACCTG     420
CGAACAAATC CAAGTGACCC CAGA                                            444
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Ala Gln Ala Val Ala Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala
1               5                  10                  15
Arg Arg Gln Met Gln Asp Ala Ala Gly Arg Arg His Phe His Ala Ser
            20                  25                  30
Gln Cys Pro Arg Pro Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser
        35                  40                  45
Ala Val Val Ile Gln Lys Ala Arg Pro Ala Lys Lys Gln Lys His Gln
    50                  55                  60
Pro Gly His Leu Arg Arg Glu Ala Tyr Ala Asp Asp Leu Pro Pro Pro
65                  70                  75                  80
Pro Val Pro Pro Pro Ala Ile Lys Ser Pro Thr Val Gln Ser Lys Ala
                85                  90                  95
```

Gln Leu Glu Val Arg Pro Val Met Val Pro Lys Leu Ala Ser Ile Glu
100 105 110
Ala Arg Thr Asp Arg Ser Ser Asp Arg Lys Gly Gly Ser Tyr Lys Gly
115 120 125
Arg Glu Ala Leu Asp Gly Arg Gln Val Thr Asp Leu Arg Thr Asn Pro
130 135 140
Ser Asp Pro Arg
145

WHAT IS CLAIMED IS:

1. An isolated Robo polypeptide comprising SEQ ID NO:2, 4, 6, 8, 10 or 12, or a polypeptide domain thereof having at least 12 consecutive residues thereof and a Robo-specific activity, wherein said domain is encoded by neither EST yq76e12 nor yq76e12.

2. An isolated polypeptide according to claim 1, wherein said activity is selected from at least one of a Robo-competitive binding, Robo-specific antigenicity and a Robo-specific immunogenicity.

3. An isolated polypeptide according to claim 1, wherein said domain comprises at least one of a Robo immunoglobulin, fibronectin or cytoplasmic motif domain.

4. A recombinant nucleic acid encoding a polypeptide according to claim 1.

5. A cell comprising a nucleic acid according to claim 4.

6. A method of making a Robo polypeptide, comprising the following steps: incubating a host cell or cellular extract containing a nucleic acid according to claim 4 under conditions whereby the polypeptide encoded by the nucleic acid is expressed and recovering the expressed polypeptide.

7. An isolated Robo polypeptide made by the method of claim 6.

8. An isolated *robo* nucleic acid comprising a strand of SEQ ID NO:1, 3, 5, 7, 9 or 11, or a fragment thereof having at least 24 consecutive bases thereof, and sufficient to specifically hybridize with a nucleic acid having the sequence defined by the corresponding opposite strand, wherein the fragment is contained in neither EST yq76e12 nor yq76e12.

9. A method for modulating cell function or morphology comprising providing the cell with an agent which modulates activity of a Robo polypeptide or function of a *robo* gene, wherein the agent comprises a polypeptide according to claim 1 or a Robo-specific antibody.

ABSTRACT OF THE DISCLOSURE

Robo1 and Robo2 polypeptides may be produced recombinantly from transformed host cells from the disclosed Robo encoding nucleic acids or purified from human cells. The invention provides isolated Robo hybridization probes and primers capable of specifically hybridizing with the disclosed Robo genes, Robo-specific binding agents such as specific antibodies, and methods of making and using the subject compositions in diagnosis, therapy and in the biopharmaceutical industry.

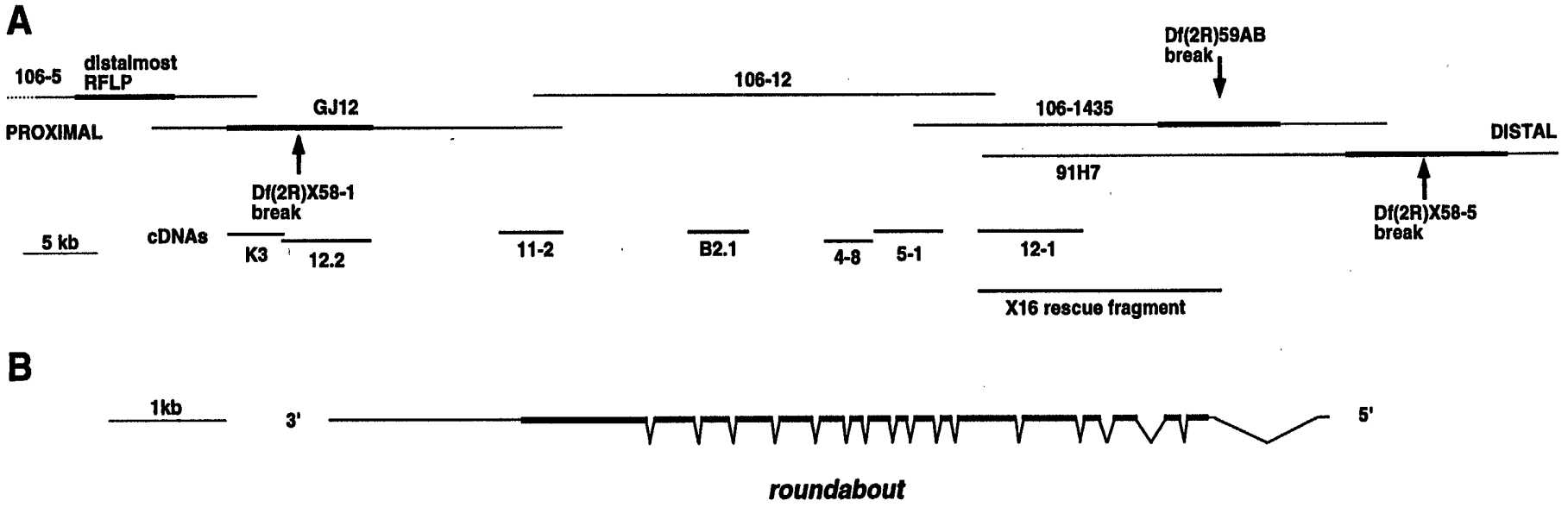

FIG. 1

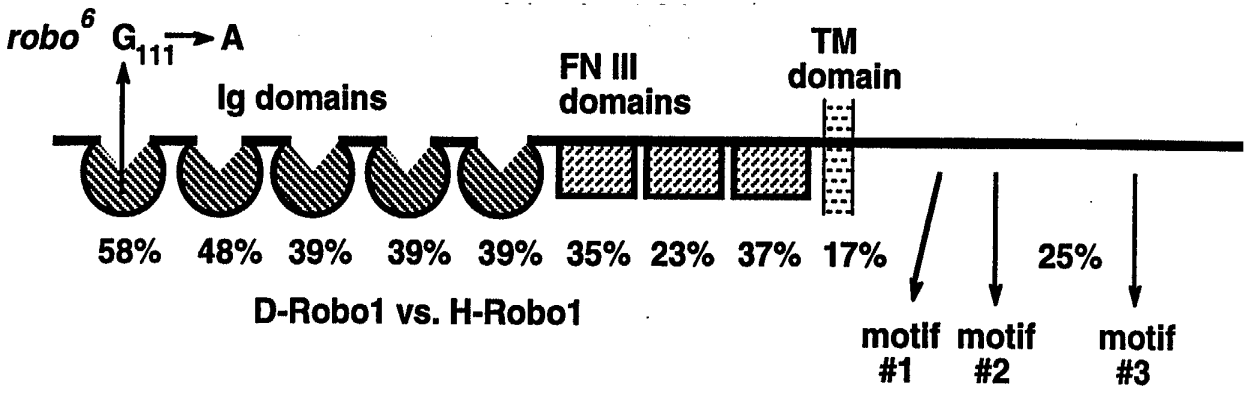

FIG. 2

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Goodman, Corey S.
Kidd, Thomas
Mitchell, Kevin
Tear, Guy

(ii) TITLE OF INVENTION: Robo: A Novel Family of Polypeptide and Nucleic Acids

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

(B) STREET: 75 DENISE DRIVE

(C) CITY: HILLSBOROUGH

(D) STATE: CALIFORNIA

(E) COUNTRY: USA

(F) ZIP: 94010

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: OSMAN, RICHARD A

(B) REGISTRATION NUMBER: 36,627

(C) REFERENCE/DOCKET NUMBER: B98-006

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 343-4341

(B) TELEFAX: (650) 343-4342

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4188 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGCATCCCA TGCATCCCGA AAACCACGCC ATCGCCCGGA GCACGAGCAC CACTAATAAC 60

CCATCTCGCA GTCGGAGCAG CAGGATGTGG CTCCTGCCCG CCTGGCTGCT CCTCGTCCTG 120

GTGGCCAGCA ATGGCCTGCC AGCAGTCAGA GGCCAGTACC AATCGCCACG TATCATCGAG 180

CATCCCACGG ATCTGGTCGT TAAGAAGAAT GAACCCGCCA CGCTCAACTG CAAAGTGGAG 240

GGCAAGCCGG AACCCACCAT TGAGTGGTTT AAGGATGGCG AACCCGTCAG CACCAACGAA 300

AAGAAATCGC ACCGCGTCCA GTTCAAGGAC GGCGCCCTCT TCTTTTACAG GACAATGCAA 360

GGCAAGAAGG AGCAGGACGG CGGAGAGTAC TGGTGCGTGG CCAAGAACCG AGTGGGCCAG 420

GCCGTTAGTC GCCATGCCTC CCTCCAGATA GCTGTTTTGC GCGACGATTT TCGCGTGGAG 480

CCCAAAGACA CGCGAGTGGC CAAAGGCGAG ACGGCTCTGC TGGAGTGTGG GCCGCCCAAA 540

GGCATTCCAG AGCCAACGCT GATTTGGATA AAGGACGGCG TTCCCTTGGA CGACCTGAAA 600

GCCATGTCGT TTGGCGCCAG CTCCCGCGTT CGAATTGTGG ACGGTGGCAA CCTGCTGATC 660

AGCAATGTGG AGCCCATTGA TGAGGGCAAC TACAAGTGCA TTGCCCAGAA TCTGGTAGGC 720

ACCCGCGAGA GCAGCTATGC CAAGCTGATT GTCCAGGTCA AACCATACTT TATGAAGGAG 780

CCCAAGGATC AGGTGATGCT CTACGGCCAG ACAGCCACTT TCCACTGCTC AGTGGGCGGT 840

GATCCGCCGC CGAAAGTGTT GTGGAAAAAG GAGGAGGGCA ATATTCCGGT GTCCAGAGCG 900

CGAATCCTTC ACGACGAGAA AAGTTTAGAG ATATCCAACA TAACGCCCAC CGATGAGGGC 960

ACCTATGTCT GCGAGGCACA CAACAATGTC GGTCAGATCA GCGCTAGGGC TTCTCTTATA 1020

GTCCACGCTC CGCCGAACTT TACGAAAAGA CCCAGTAACA AGAAAGTGGG ACTAAATGGG 1080

GTTGTCCAAC TACCTTGCAT GGCCTCCGGA AACCCTCCGC CGTCTGTATT CTGGACCAAG 1140

GAAGGAGTAT CCACTCTTAT GTTCCCAAAT AGTTCGCACG GAAGGCAGTA TGTGGCTGCC 1200

GATGGAACTC TGCAGATTAC GGATGTGCGG CAGGAAGACG AAGGCTACTA TGTGTGTTCC 1260

GCTTTCAGTG TAGTCGATTC CTCTACAGTA CGGGTTTTCC TGCAAGTCAG CTCGGTAGAC 1320

GAGCGTCCAC CTCCGATTAT TCAAATCGGA CCTGCCAATC AAACACTGCC CAAGGGATCA 1380

GTTGCTACTT TACCCTGTCG GGCCACTGGA AATCCCAGTC CCCGTATCAA GTGGTTCCAC 1440

GATGGACATG CCGTACAAGC GGGCAATCGA TACAGCATCA TCCAAGGAAG CTCACTGAGA 1500

GTCGATGACC TTCAACTAAG TGACTCTGGT ACCTACACCT GCACTGCATC TGGCGAACGA 1560

GGAGAAACTT CCTGGGCTGC CACACTAACG GTGGAAAAAC CCGGTTCTAC ATCTCTTCAC 1620

CGGGCAGCTG ATCCTAGCAC TTATCCTGCT CCTCCAGGAA CACCTAAAGT CCTGAATGTC 1680

AGTCGCACCA GCATTAGTCT TCGTTGGGCT AAAAGCCAAG AGAAACCCGG AGCTGTGGGC 1740

CCAATCATTG GATACACTGT AGAGTACTTC AGTCCGGATC TGCAAACTGG TTGGATTGTG 1800

GCTGCCCATC GAGTCGGCGA CACTCAAGTC ACTATCTCGG GTCTCACTCC TGGCACTTCG 1860

TATGTGTTCC TAGTTAGAGC TGAGAATACT CAGGGTATTT CTGTGCCTTC CGGCTTATCA 1920

AATGTTATTA AAACCATTGA GGCAGATTTC GATGCAGCTT CTGCCAATGA TTTGTCAGCA 1980

GCTCGAACTT TGCTGACAGG AAAGTCGGTG GAGCTAATAG ATGCCTCGGC TATCAATGCT 2040

AGTGCCGTTA GACTTGAGTG GATGCTCCAC GTGAGCGCTG ATGAGAAATA CGTAGAGGGC 2100

CTGCGCATAC ACTATAAGGA TGCCAGTGTA CCATCCGCAC AGTATCACTC GATCACTGTT 2160

ATGGATGCCT CTGCAGAATC GTTTGTGGTG GGAAACCTTA AGAAGTACAC CAAGTATGAG 2220

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CAAACAGCCG GTTGGGTGCG TTGGACTCCG CCACCCTCCC AGCACCACAA TGGCAATTTG 2400

TATGGCTACA AGATTGAGGT CAGCGCCGGT AACACCATGA AGGTGCTGGC CAATATGACT 2460

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ATAACCGCAT TAAATATCAA TAGCAAAGAG AGCCTTTGGA TAGACCATCA TCGTGGATGG 2940

CGAACTGCCG ATACTGACAA AGACTCAGGA TTAAGCGAAT CGAAGCTACT ATCCCACGTT 3000

AACAGCAGTC AATCCAACTA CAATAACTCC GATGGAGGAA CCGATTATGC AGAAGTTGAC 3060

ACCCGTAACC TTACCACCTT CTACAATTGT CGCAAGAGCC CCGATAATCC CACGCCGTAC 3120

GCCACCACTA TGATCATTGG TACCTCTTCC AGTGAGACCT GCACCAAGAC AACATCTATA 3180

AGTGCCGATA AGGACTCGGG AACTCATTCG CCCTATTCTG ACGCATTTGC CGGTCAGGTG 3240

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TCAGAGTTTC TACCCCCGCC GCCAGAACAC CCACCTCCGT CTTCTACCTA TGGATACGCA 3360

CAAGGATCTC CTGAATCTTC GCGGAAGAGC TCCAAAAGCG CAGGTTCCGG CATTTCTACA 3420

AATCAAAGCA TTCTGAACGC ATCCATACAC AGCAGCTCCT CGGGCGGCTT TTCAGCTTGG 3480

GGAGTATCGC CCCAATATGC TGTCGCCTGT CCACCGGAAA ACGTTTATAG CAATCCGCTG 3540

TCGGCAGTGG CTGGCGGCAC CCAGAACCGC TATCAGATAA CGCCCACAAA CCAACATCCG 3600

CCACAGTTAC CGGCCTACTT TGCCACCACG GGTCCAGGAG GAGCTGTACC ACCCAACCAC 3660

CTGCCATTTG CCACACAGCG TCATGCAGCC AGCGAGTACC AGGCTGGACT GAATGCAGCG 3720

CGATGTGCCC AAAGCCGCGC CTGCAACAGC TGCGATGCCT TGGCCACACC CTCGCCCATG 3780

CAACCCCCAC CGCCAGTTCC CGTACCCGAG GGCTGGTACC AACCGGTGCA TCCCAATAGC 3840

CACCCGATGC ACCCGACCTC CTCCAACCAC CAGATCTACC AGTGCTCCTC CGAGTGCTCG 3900

GATCACTCGA GGAGCTCGCA GAGTCACAAG CGGCAGCTGC AGCTCGAGGA GCACGGCAGC 3960

AGTGCCAAAC AACGCGGAGG ACACCACCGT CGACGAGCCC CGGTGGTGCA GCCGTGCATG 4020

GAGAGCGAGA ACGAGAACAT GCTGGCGGAG TACGAGCAGC GCCAGTACAC CAGCGATTGC 4080

TGCAATAGCT CCCGCGAGGG CGACACCTGC TCCTGCAGCG AGGGATCCTG TCTTTACGCC 4140

GAGGCGGGCG AGCCGGCGCC TCGTCAAATG ACTGCTAAGA ACACCTAA 4188

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1395 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met His Pro Met His Pro Glu Asn His Ala Ile Ala Arg Ser Thr Ser
1               5                  10                  15
Thr Thr Asn Asn Pro Ser Arg Ser Arg Ser Ser Arg Met Trp Leu Leu
            20                  25                  30
Pro Ala Trp Leu Leu Leu Val Leu Val Ala Ser Asn Gly Leu Pro Ala
        35                  40                  45
Val Arg Gly Gln Tyr Gln Ser Pro Arg Ile Ile Glu His Pro Thr Asp
    50                  55                  60
Leu Val Val Lys Lys Asn Glu Pro Ala Thr Leu Asn Cys Lys Val Glu
65                  70                  75                  80
Gly Lys Pro Glu Pro Thr Ile Glu Trp Phe Lys Asp Gly Glu Pro Val
                85                  90                  95
Ser Thr Asn Glu Lys Lys Ser His Arg Val Gln Phe Lys Asp Gly Ala
            100                 105                 110
Leu Phe Phe Tyr Arg Thr Met Gln Gly Lys Lys Glu Gln Asp Gly Gly
        115                 120                 125
Glu Tyr Trp Cys Val Ala Lys Asn Arg Val Gly Gln Ala Val Ser Arg
    130                 135                 140
His Ala Ser Leu Gln Ile Ala Val Leu Arg Asp Asp Phe Arg Val Glu
145                 150                 155                 160
Pro Lys Asp Thr Arg Val Ala Lys Gly Glu Thr Ala Leu Leu Glu Cys
                165                 170                 175
Gly Pro Pro Lys Gly Ile Pro Glu Pro Thr Leu Ile Trp Ile Lys Asp
            180                 185                 190
Gly Val Pro Leu Asp Asp Leu Lys Ala Met Ser Phe Gly Ala Ser Ser
        195                 200                 205
Arg Val Arg Ile Val Asp Gly Gly Asn Leu Leu Ile Ser Asn Val Glu
    210                 215                 220
Pro Ile Asp Glu Gly Asn Tyr Lys Cys Ile Ala Gln Asn Leu Val Gly
225                 230                 235                 240
Thr Arg Glu Ser Ser Tyr Ala Lys Leu Ile Val Gln Val Lys Pro Tyr
                245                 250                 255
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Phe Met Lys Glu Pro Lys Asp Gln Val Met Leu Tyr Gly Gln Thr Ala
260 265 270
Thr Phe His Cys Ser Val Gly Gly Asp Pro Pro Pro Lys Val Leu Trp
275 280 285
Lys Lys Glu Glu Gly Asn Ile Pro Val Ser Arg Ala Arg Ile Leu His
290 295 300
Asp Glu Lys Ser Leu Glu Ile Ser Asn Ile Thr Pro Thr Asp Glu Gly
305 310 315 320
Thr Tyr Val Cys Glu Ala His Asn Asn Val Gly Gln Ile Ser Ala Arg
325 330 335
Ala Ser Leu Ile Val His Ala Pro Pro Asn Phe Thr Lys Arg Pro Ser
340 345 350
Asn Lys Lys Val Gly Leu Asn Gly Val Val Gln Leu Pro Cys Met Ala
355 360 365
Ser Gly Asn Pro Pro Pro Ser Val Phe Trp Thr Lys Glu Gly Val Ser
370 375 380
Thr Leu Met Phe Pro Asn Ser Ser His Gly Arg Gln Tyr Val Ala Ala
385 390 395 400
Asp Gly Thr Leu Gln Ile Thr Asp Val Arg Gln Glu Asp Glu Gly Tyr
405 410 415
Tyr Val Cys Ser Ala Phe Ser Val Val Asp Ser Ser Thr Val Arg Val
420 425 430
Phe Leu Gln Val Ser Ser Val Asp Glu Arg Pro Pro Pro Ile Ile Gln
435 440 445
Ile Gly Pro Ala Asn Gln Thr Leu Pro Lys Gly Ser Val Ala Thr Leu
450 455 460
Pro Cys Arg Ala Thr Gly Asn Pro Ser Pro Arg Ile Lys Trp Phe His
465 470 475 480
Asp Gly His Ala Val Gln Ala Gly Asn Arg Tyr Ser Ile Ile Gln Gly
485 490 495
Ser Ser Leu Arg Val Asp Asp Leu Gln Leu Ser Asp Ser Gly Thr Tyr
500 505 510
Thr Cys Thr Ala Ser Gly Glu Arg Gly Glu Thr Ser Trp Ala Ala Thr
515 520 525
Leu Thr Val Glu Lys Pro Gly Ser Thr Ser Leu His Arg Ala Ala Asp
530 535 540
Pro Ser Thr Tyr Pro Ala Pro Pro Gly Thr Pro Lys Val Leu Asn Val
545 550 555 560

Ser Arg Thr Ser Ile Ser Leu Arg Trp Ala Lys Ser Gln Glu Lys Pro
565 570 575
Gly Ala Val Gly Pro Ile Ile Gly Tyr Thr Val Glu Tyr Phe Ser Pro
580 585 590
Asp Leu Gln Thr Gly Trp Ile Val Ala Ala His Arg Val Gly Asp Thr
595 600 605
Gln Val Thr Ile Ser Gly Leu Thr Pro Gly Thr Ser Tyr Val Phe Leu
610 615 620
Val Arg Ala Glu Asn Thr Gln Gly Ile Ser Val Pro Ser Gly Leu Ser
625 630 635 640
Asn Val Ile Lys Thr Ile Glu Ala Asp Phe Asp Ala Ala Ser Ala Asn
645 650 655
Asp Leu Ser Ala Ala Arg Thr Leu Leu Thr Gly Lys Ser Val Glu Leu
660 665 670
Ile Asp Ala Ser Ala Ile Asn Ala Ser Ala Val Arg Leu Glu Trp Met
675 680 685
Leu His Val Ser Ala Asp Glu Lys Tyr Val Glu Gly Leu Arg Ile His
690 695 700
Tyr Lys Asp Ala Ser Val Pro Ser Ala Gln Tyr His Ser Ile Thr Val
705 710 715 720
Met Asp Ala Ser Ala Glu Ser Phe Val Val Gly Asn Leu Lys Lys Tyr
725 730 735
Thr Lys Tyr Glu Phe Phe Leu Thr Pro Phe Phe Glu Thr Ile Glu Gly
740 745 750
Gln Pro Ser Asn Ser Lys Thr Ala Leu Thr Tyr Glu Asp Val Pro Ser
755 760 765
Ala Pro Pro Asp Asn Ile Gln Ile Gly Met Tyr Asn Gln Thr Ala Gly
770 775 780
Trp Val Arg Trp Thr Pro Pro Pro Ser Gln His His Asn Gly Asn Leu
785 790 795 800
Tyr Gly Tyr Lys Ile Glu Val Ser Ala Gly Asn Thr Met Lys Val Leu
805 810 815
Ala Asn Met Thr Leu Asn Ala Thr Thr Thr Ser Val Leu Leu Asn Asn
820 825 830
Leu Thr Thr Gly Ala Val Tyr Ser Val Arg Leu Asn Ser Phe Thr Lys
835 840 845
Ala Gly Asp Gly Pro Tyr Ser Lys Pro Ile Ser Leu Phe Met Asp Pro
850 855 860

Thr His His Val His Pro Pro Arg Ala His Pro Ser Gly Thr His Asp
865 870 875 880
Gly Arg His Glu Gly Gln Asp Leu Thr Tyr His Asn Asn Gly Asn Ile
885 890 895
Pro Pro Gly Asp Ile Asn Pro Thr Thr His Lys Lys Thr Thr Asp Tyr
900 905 910
Leu Ser Gly Pro Trp Leu Met Val Leu Val Cys Ile Val Leu Leu Val
915 920 925
Leu Val Ile Ser Ala Ala Ile Ser Met Val Tyr Phe Lys Arg Lys His
930 935 940
Gln Met Thr Lys Glu Leu Gly His Leu Ser Val Val Ser Asp Asn Glu
945 950 955 960
Ile Thr Ala Leu Asn Ile Asn Ser Lys Glu Ser Leu Trp Ile Asp His
965 970 975
His Arg Gly Trp Arg Thr Ala Asp Thr Asp Lys Asp Ser Gly Leu Ser
980 985 990
Glu Ser Lys Leu Leu Ser His Val Asn Ser Ser Gln Ser Asn Tyr Asn
995 1000 1005
Asn Ser Asp Gly Gly Thr Asp Tyr Ala Glu Val Asp Thr Arg Asn Leu
1010 1015 1020
Thr Thr Phe Tyr Asn Cys Arg Lys Ser Pro Asp Asn Pro Thr Pro Tyr
1025 1030 1035 1040
Ala Thr Thr Met Ile Ile Gly Thr Ser Ser Ser Glu Thr Cys Thr Lys
1045 1050 1055
Thr Thr Ser Ile Ser Ala Asp Lys Asp Ser Gly Thr His Ser Pro Tyr
1060 1065 1070
Ser Asp Ala Phe Ala Gly Gln Val Pro Ala Val Pro Val Val Lys Ser
1075 1080 1085
Asn Tyr Leu Gln Tyr Pro Val Glu Pro Ile Asn Trp Ser Glu Phe Leu
1090 1095 1100
Pro Pro Pro Pro Glu His Pro Pro Pro Ser Ser Thr Tyr Gly Tyr Ala
1105 1110 1115 1120
Gln Gly Ser Pro Glu Ser Ser Arg Lys Ser Ser Lys Ser Ala Gly Ser
1125 1130 1135
Gly Ile Ser Thr Asn Gln Ser Ile Leu Asn Ala Ser Ile His Ser Ser
1140 1145 1150
Ser Ser Gly Gly Phe Ser Ala Trp Gly Val Ser Pro Gln Tyr Ala Val
1155 1160 1165

Ala Cys Pro Pro Glu Asn Val Tyr Ser Asn Pro Leu Ser Ala Val Ala
1170 1175 1180

Gly Gly Thr Gln Asn Arg Tyr Gln Ile Thr Pro Thr Asn Gln His Pro
1185 1190 1195 1200

Pro Gln Leu Pro Ala Tyr Phe Ala Thr Thr Gly Pro Gly Gly Ala Val
1205 1210 1215

Pro Pro Asn His Leu Pro Phe Ala Thr Gln Arg His Ala Ala Ser Glu
1220 1225 1230

Tyr Gln Ala Gly Leu Asn Ala Ala Arg Cys Ala Gln Ser Arg Ala Cys
1235 1240 1245

Asn Ser Cys Asp Ala Leu Ala Thr Pro Ser Pro Met Gln Pro Pro Pro
1250 1255 1260

Pro Val Pro Val Pro Glu Gly Trp Tyr Gln Pro Val His Pro Asn Ser
1265 1270 1275 1280

His Pro Met His Pro Thr Ser Ser Asn His Gln Ile Tyr Gln Cys Ser
1285 1290 1295

Ser Glu Cys Ser Asp His Ser Arg Ser Ser Gln Ser His Lys Arg Gln
1300 1305 1310

Leu Gln Leu Glu Glu His Gly Ser Ser Ala Lys Gln Arg Gly Gly His
1315 1320 1325

His Arg Arg Arg Ala Pro Val Val Gln Pro Cys Met Glu Ser Glu Asn
1330 1335 1340

Glu Asn Met Leu Ala Glu Tyr Glu Gln Arg Gln Tyr Thr Ser Asp Cys
1345 1350 1355 1360

Cys Asn Ser Ser Arg Glu Gly Asp Thr Cys Ser Cys Ser Glu Gly Ser
1365 1370 1375

Cys Leu Tyr Ala Glu Ala Gly Glu Pro Ala Pro Arg Gln Met Thr Ala
1380 1385 1390

Lys Asn Thr
1395

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTGAAAATC CACGCATCAT CGAGCATCCC ATGGACACGA CGGTGCCAAA AAATGATCCA 60

TTTACGTTTA ATTGCCAGGC CGAGGGCAAT CCAACACCAA CCATTCAATG GTTTAAGGAC 120

GGTCGCGAAC TGAAGACGGA TACGGGTTCG CATCGCATAA TGCTGCCCGC CGGGGGTCTA 180

TTCTTTCTCA AGGTTATCCA CTCACGTAGA GAGAGCGATG CGGGCACTTA CTGGTGCGAG 240

GCCAAAAACG AGTTTGGAGT GGCACGGTCC AGGAATGCAA CGTTGCAAGT GGCAGTTCTC 300

CGCGACGAAT TCCGTTTGGA GCCGGCAAAT ACCCGCGTGG CCCAAGGCGA GGTGGCCCTG 360

ATGGAATGCG GTGCCCCCCG AGGATCTCCG GAGCCGCAAA TCTCGTGGCG CAAGAACGGC 420

CAGACCCTGA ATCTTGTCGG GAACAAGCGG ATTCGCATTG TCGACGGTGG CAATCTGGCC 480

ATCCAGGAAG CCCGCCAATC GGACGACGGA CGCTACCAGT GTGTGGTCAA GAATGTGGTT 540

GGCACCCGGG AGTCGGCCAC CGCTTTTCTT AAAGTGCATG TACGTCCATT CCTCATCCGA 600

GGACCCCAGA ATCAGACGGC GGTGGTGGGC AGCTCGGTGG TCTTCCAGTG CCGCATCGGA 660

GGCGATCCCC TGCCTGATGT CCTGTGGCGA CGCACTGCCT CCGGCGGCAA TATGCCACTG 720

CGTAAGTTTT CTTGGCTTCA TTCAGCTTCA GGTCGTGTGC ACGTACTTGA GGACCGCAGT 780

CTGAAGCTGG ACGACGTTAC TCTGGAGGAC ATGGGCGAGT ACACTTGCGA GGCGGACAAT 840

GCGGTGGGCG GCATCACGGC CACTGGCATC CTCACCGTTC ACGCTCCCCC CAAATTTGTG 900

ATACGCCCCA AGAATCAGCT GGTGGAGATC GGTGATGAAG TGCTGTTCGA GTGCCAAGCG 960

AATGGACATC CCCGACCAAC GCTCTACTGG TCGGTGGAGG GCAACAGCTC CCTGCTGCTC 1020

CCCGGCTATC GGGATGGCCG CATGGAAGTG ACCCTGACGC CCGAGGGGCG CTCGGTGCTC 1080

TCGATAGCTC GATTTGCCCG TGAGGATTCC GGAAAGGTGG TCACTTGCAA CGCCCTGAAC 1140

GCCGTGGGCA GCGTCAGCAG TCGGACTGTG GTCAGTGTGG ATACGCAATT CGAGCTGCCA 1200

CCGCCGATTA TCGAACAGGG GCCCGTGAAT CAAACGTTGC CCGTTAAATC AATTGTGGTT 1260

CTGCCATGCC GAACTCTGGG CACTCCAGTG CCACAGGTCT CTTGGTACCT GGATGGCATA 1320

CCCATCGATG TGCAGGAGCA CGAGCGGCGG AATCTTTCGG ACGCTGGAGC CTTAACCATT 1380

TCGGATCTTC AGCGCCACGA GGATGAAGGC TTGTACACCT GCGTGGCCAG CAATCGCAAC 1440

GGAAAATCCT CTTGGAGTGG TTACCTTCGT CTGGACACCC CGACAAATCC GAATATCAAG 1500

TTCTTCAGAG CCCCAGAACT TTCCACCTAC CCAGGGCCGC CAGGAAAACC GCAAATGGTG 1560

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TACTTCTTTC TAATTCGAGC CGAGAACTCC CATGGCTTAT CACTGCCCAG TCCGATGTCG 1800

GAACCCATTA CGGTGGGAAC GCGCTACTTC AATAGTGGTC TGGATCTGAG CGAGGCTCGT 1860

GCCAGTCTGC TGTCCGGAGA TGTTGTGGAG CTGAGCAACG CCAGTGTGGT GGACTCCACT 1920

AGCATGAAAC TCACCTGGCA GATCATCAAT GGCAAATACG TCGAGGGCTT CTATGTCTAT 1980

GCGAGACAGT TGCCAAATCC AATAGTCAAC AATCCGGCGC CCGTTACTAG CAATACCAAT 2040

CCGCTGCTGG GCTCTACATC CACATCCGCA TCCGCATCCG CCTCGGCATC GGCATTGATT 2100

TCGACAAAGC CAAATATTGC AGCTGCCGGC AAACGTGATG GGGAGACAAA CCAGAGTGGA 2160

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GTGCCATTTT ACAAATCCGT CGAGGGCAAG CCGTCGAATT CGCGCATCGC TCGCACCCTT 2340

GAAGATGTTC CCTCTGAGGC ACCATATGGA ATGGAGGCTC TGCTGTTGAA CTCCTCCGCG 2400

GTCTTCCTCA AATGGAAGGC ACCAGAACTC AAGGATCGGC ATGGTGTTCT CTTGAACTAT 2460

CATGTTATAG TCCGAGGTAT TGACACTGCC CACAATTTCT CACGCATTTT GACAAATGTC 2520

ACCATCGATG CCGCTTCGCC TACTCTGGTT TTGGCCAATC TCACCGAAGG CGTCATGTAC 2580

ACCGTGGGCG TGGCGGCCGG AAATAACGCT GGAGTTGGTC CTTATTGTGT CCCAGCTACT 2640

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AACGATGTGC TGACGCAGCC CTGGTTCATA ATACTCCTGG GCGCCATCCT GGCCGTTCTT 2760

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GCCCTAAATA CAATGCGTGG CAATCACACG AGCGACGTGC TCAAAATGCC GAGTCTATCG 2880

GCGCGCAATG GAAACGGCTA CTGGCTGGAC TCCTCCACCG GCGGAATGGT GTGGCGTCCC 2940

TCGCCCGGCG GCGACTCGCT GGAGATGCAA AAGGATCACA TCGCCGACTA TGCGCCGGTC 3000

TGCGGTGCCC CCGGTTCTCC GGCCGGCGGT GGCACCTCTT CCGGTGGATC CGGTGGCGCG 3060

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CCAGTGCCCG GCTATGGGCT CCAGCGCCCA ATGCACCCAC ACTACCAGCA GCAGCAGCAT 3360

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CACATCCACA TCACCGAGAA CAAGCTGAGC AACTGCCACA CCTATGAGGC GGCTCCTGGC 3600

GCCAAGCAGT CCTCGCCGAT ATCCTCGCAG TTCGCCAGCG TGAGGCGGCA GCAGCTGCCG 3660

CCCAACTGCA GCATCGGCAG GGAAAGTGCC CGCTTCAAGG TGCTAAACAC GGATCAGGGC 3720

AAGAACCAGC AGAATCTCCT GGATCTCGAC GGCTCCTCGA TGTGCTACAA CGGTCTGGCA 3780

GACTCGGGCT GCGGTGGATC TCCCTCCCCG ATGGCCATGC TGATGTCGCA CGAGGACGAG 3840

CACGCGCTGT ACCACACGGC GGATGGGGAT CTGGACGACA TGGAACGACT GTACGTCAAG 3900

GTGGACGAGC AGCAGCCTCC ACAGCAGCAG CAGCAGCTGA TTCCCCTGGT CCCACAGCAT 3960

CCGGCGGAAG GTCACCTGCA GTCCTGGCGG AATCAGAGCA CGCGGAGCAG TCGGAAGAAC 4020

GGCCAGGAAT GCATCAAGGA ACCCAGCGAG TTGATCTACG CTCCGGGAAG CGTGGCCAGC 4080

GAACGGAGCC TCCTCAGCAA CTCGGGTAGC GGCACCAGCA GCCAGCCAGC TGGCCACAAT 4140

GTCTGA 4146

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1381 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gly Glu Asn Pro Arg Ile Ile Glu His Pro Met Asp Thr Thr Val Pro
1 5 10 15

Lys Asn Asp Pro Phe Thr Phe Asn Cys Gln Ala Glu Gly Asn Pro Thr
20 25 30

Pro Thr Ile Gln Trp Phe Lys Asp Gly Arg Glu Leu Lys Thr Asp Thr
35 40 45

Gly Ser His Arg Ile Met Leu Pro Ala Gly Gly Leu Phe Phe Leu Lys
50 55 60

Val Ile His Ser Arg Arg Glu Ser Asp Ala Gly Thr Tyr Trp Cys Glu
65 70 75 80

Ala Lys Asn Glu Phe Gly Val Ala Arg Ser Arg Asn Ala Thr Leu Gln
85 90 95

Val Ala Val Leu Arg Asp Glu Phe Arg Leu Glu Pro Ala Asn Thr Arg
100 105 110

Val Ala Gln Gly Glu Val Ala Leu Met Glu Cys Gly Ala Pro Arg Gly
115 120 125

Ser Pro Glu Pro Gln Ile Ser Trp Arg Lys Asn Gly Gln Thr Leu Asn
130 135 140

Leu Val Gly Asn Lys Arg Ile Arg Ile Val Asp Gly Gly Asn Leu Ala
145 150 155 160

Ile Gln Glu Ala Arg Gln Ser Asp Asp Gly Arg Tyr Gln Cys Val Val
165 170 175

Lys Asn Val Val Gly Thr Arg Glu Ser Ala Thr Ala Phe Leu Lys Val
180 185 190

His Val Arg Pro Phe Leu Ile Arg Gly Pro Gln Asn Gln Thr Ala Val
195 200 205

Val Gly Ser Ser Val Val Phe Gln Cys Arg Ile Gly Gly Asp Pro Leu
210 215 220

Pro Asp Val Leu Trp Arg Arg Thr Ala Ser Gly Gly Asn Met Pro Leu
225 230 235 240

Arg Lys Phe Ser Trp Leu His Ser Ala Ser Gly Arg Val His Val Leu
245 250 255

Glu Asp Arg Ser Leu Lys Leu Asp Asp Val Thr Leu Glu Asp Met Gly
260 265 270

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Glu Tyr Thr Cys Glu Ala Asp Asn Ala Val Gly Gly Ile Thr Ala Thr
        275                 280                 285
Gly Ile Leu Thr Val His Ala Pro Pro Lys Phe Val Ile Arg Pro Lys
    290                 295                 300
Asn Gln Leu Val Glu Ile Gly Asp Glu Val Leu Phe Glu Cys Gln Ala
305                 310                 315                 320
Asn Gly His Pro Arg Pro Thr Leu Tyr Trp Ser Val Glu Gly Asn Ser
                325                 330                 335
Ser Leu Leu Leu Pro Gly Tyr Arg Asp Gly Arg Met Glu Val Thr Leu
            340                 345                 350
Thr Pro Glu Gly Arg Ser Val Leu Ser Ile Ala Arg Phe Ala Arg Glu
        355                 360                 365
Asp Ser Gly Lys Val Val Thr Cys Asn Ala Leu Asn Ala Val Gly Ser
    370                 375                 380
Val Ser Ser Arg Thr Val Val Ser Val Asp Thr Gln Phe Glu Leu Pro
385                 390                 395                 400
Pro Pro Ile Ile Glu Gln Gly Pro Val Asn Gln Thr Leu Pro Val Lys
                405                 410                 415
Ser Ile Val Val Leu Pro Cys Arg Thr Leu Gly Thr Pro Val Pro Gln
            420                 425                 430
Val Ser Trp Tyr Leu Asp Gly Ile Pro Ile Asp Val Gln Glu His Glu
        435                 440                 445
Arg Arg Asn Leu Ser Asp Ala Gly Ala Leu Thr Ile Ser Asp Leu Gln
    450                 455                 460
Arg His Glu Asp Glu Gly Leu Tyr Thr Cys Val Ala Ser Asn Arg Asn
465                 470                 475                 480
Gly Lys Ser Ser Trp Ser Gly Tyr Leu Arg Leu Asp Thr Pro Thr Asn
                485                 490                 495
Pro Asn Ile Lys Phe Phe Arg Ala Pro Glu Leu Ser Thr Tyr Pro Gly
            500                 505                 510
Pro Pro Gly Lys Pro Gln Met Val Glu Lys Gly Glu Asn Ser Val Thr
        515                 520                 525
Leu Ser Trp Thr Arg Ser Asn Lys Val Gly Gly Ser Ser Leu Val Gly
    530                 535                 540
Tyr Val Ile Glu Met Phe Gly Lys Asn Glu Thr Asp Gly Trp Val Ala
545                 550                 555                 560
Val Gly Thr Arg Val Gln Asn Thr Thr Phe Thr Gln Thr Gly Leu Leu
                565                 570                 575
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Pro Gly Val Asn Tyr Phe Phe Leu Ile Arg Ala Glu Asn Ser His Gly
            580                 585                 590
Leu Ser Leu Pro Ser Pro Met Ser Glu Pro Ile Thr Val Gly Thr Arg
        595                 600                 605
Tyr Phe Asn Ser Gly Leu Asp Leu Ser Glu Ala Arg Ala Ser Leu Leu
    610                 615                 620
Ser Gly Asp Val Val Glu Leu Ser Asn Ala Ser Val Val Asp Ser Thr
625                 630                 635                 640
Ser Met Lys Leu Thr Trp Gln Ile Ile Asn Gly Lys Tyr Val Glu Gly
                645                 650                 655
Phe Tyr Val Tyr Ala Arg Gln Leu Pro Asn Pro Ile Val Asn Asn Pro
            660                 665                 670
Ala Pro Val Thr Ser Asn Thr Asn Pro Leu Leu Gly Ser Thr Ser Thr
        675                 680                 685
Ser Ala Ser Ala Ser Ala Ser Ala Ser Ala Leu Ile Ser Thr Lys Pro
    690                 695                 700
Asn Ile Ala Ala Ala Gly Lys Arg Asp Gly Glu Thr Asn Gln Ser Gly
705                 710                 715                 720
Gly Gly Ala Pro Thr Pro Leu Asn Thr Lys Tyr Arg Met Leu Thr Ile
                725                 730                 735
Leu Asn Gly Gly Gly Ala Ser Ser Cys Thr Ile Thr Gly Leu Val Gln
            740                 745                 750
Tyr Thr Leu Tyr Glu Phe Phe Ile Val Pro Phe Tyr Lys Ser Val Glu
        755                 760                 765
Gly Lys Pro Ser Asn Ser Arg Ile Ala Arg Thr Leu Glu Asp Val Pro
    770                 775                 780
Ser Glu Ala Pro Tyr Gly Met Glu Ala Leu Leu Leu Asn Ser Ser Ala
785                 790                 795                 800
Val Phe Leu Lys Trp Lys Ala Pro Glu Leu Lys Asp Arg His Gly Val
                805                 810                 815
Leu Leu Asn Tyr His Val Ile Val Arg Gly Ile Asp Thr Ala His Asn
            820                 825                 830
Phe Ser Arg Ile Leu Thr Asn Val Thr Ile Asp Ala Ala Ser Pro Thr
        835                 840                 845
Leu Val Leu Ala Asn Leu Thr Glu Gly Val Met Tyr Thr Val Gly Val
    850                 855                 860
Ala Ala Gly Asn Asn Ala Gly Val Gly Pro Tyr Cys Val Pro Ala Thr
865                 870                 875                 880
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Leu Arg Leu Asp Pro Ile Thr Lys Arg Leu Asp Pro Phe Ile Asn Gln
885 890 895
Arg Asp His Val Asn Asp Val Leu Thr Gln Pro Trp Phe Ile Ile Leu
900 905 910
Leu Gly Ala Ile Leu Ala Val Leu Met Leu Ser Phe Gly Ala Met Val
915 920 925
Phe Val Lys Arg Lys His Met Met Met Lys Gln Ser Ala Leu Asn Thr
930 935 940
Met Arg Gly Asn His Thr Ser Asp Val Leu Lys Met Pro Ser Leu Ser
945 950 955 960
Ala Arg Asn Gly Asn Gly Tyr Trp Leu Asp Ser Ser Thr Gly Gly Met
965 970 975
Val Trp Arg Pro Ser Pro Gly Gly Asp Ser Leu Glu Met Gln Lys Asp
980 985 990
His Ile Ala Asp Tyr Ala Pro Val Cys Gly Ala Pro Gly Ser Pro Ala
995 1000 1005
Gly Gly Gly Thr Ser Ser Gly Gly Ser Gly Gly Ala Gly Ser Gly Ala
1010 1015 1020
Ser Gly Gly Asp Asp Ile His Gly Gly His Gly Ser Glu Arg Asn Gln
1025 1030 1035 1040
Gln Arg Tyr Val Gly Glu Tyr Ser Asn Ile Pro Thr Asp Tyr Ala Glu
1045 1050 1055
Val Ser Ser Phe Gly Lys Ala Pro Ser Glu Tyr Gly Arg His Gly Asn
1060 1065 1070
Ala Ser Pro Ala Pro Tyr Ala Thr Ser Ser Ile Leu Ser Pro His Gln
1075 1080 1085
Gln Gln Gln Gln Gln Gln Pro Arg Tyr Gln Gln Arg Pro Val Pro Gly
1090 1095 1100
Tyr Gly Leu Gln Arg Pro Met His Pro His Tyr Gln Gln Gln Gln His
1105 1110 1115 1120
Gln Gln Gln Gln Ala Gln Gln Thr His Gln Gln His Gln Ala Leu Gln
1125 1130 1135
Gln His Gln Gln Leu Pro Pro Ser Asn Ile Tyr Gln Gln Met Ser Thr
1140 1145 1150
Thr Ser Glu Ile Tyr Pro Thr Asn Thr Gly Pro Ser Arg Ser Val Tyr
1155 1160 1165
Ser Glu Gln Tyr Tyr Tyr Pro Lys Asp Lys Gln Arg His Ile His Ile
1170 1175 1180

Thr Glu Asn Lys Leu Ser Asn Cys His Thr Tyr Glu Ala Ala Pro Gly
1185 1190 1195 1200

Ala Lys Gln Ser Ser Pro Ile Ser Ser Gln Phe Ala Ser Val Arg Arg
1205 1210 1215

Gln Gln Leu Pro Pro Asn Cys Ser Ile Gly Arg Glu Ser Ala Arg Phe
1220 1225 1230

Lys Val Leu Asn Thr Asp Gln Gly Lys Asn Gln Gln Asn Leu Leu Asp
1235 1240 1245

Leu Asp Gly Ser Ser Met Cys Tyr Asn Gly Leu Ala Asp Ser Gly Cys
1250 1255 1260

Gly Gly Ser Pro Ser Pro Met Ala Met Leu Met Ser His Glu Asp Glu
1265 1270 1275 1280

His Ala Leu Tyr His Thr Ala Asp Gly Asp Leu Asp Asp Met Glu Arg
1285 1290 1295

Leu Tyr Val Lys Val Asp Glu Gln Gln Pro Pro Gln Gln Gln Gln Gln
1300 1305 1310

Leu Ile Pro Leu Val Pro Gln His Pro Ala Glu Gly His Leu Gln Ser
1315 1320 1325

Trp Arg Asn Gln Ser Thr Arg Ser Ser Arg Lys Asn Gly Gln Glu Cys
1330 1335 1340

Ile Lys Glu Pro Ser Glu Leu Ile Tyr Ala Pro Gly Ser Val Ala Ser
1345 1350 1355 1360

Glu Arg Ser Leu Leu Ser Asn Ser Gly Ser Gly Thr Ser Ser Gln Pro
1365 1370 1375

Ala Gly His Asn Val
1380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3894 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGTACTATC TAGGTTTTTA CCACACTCAC ACACACACAC ACACATACAT AAATTTTGAT 60

AAAATTCCTA ATGCCTCAAA TCTCGCTCCC GTGATAATCG AACATCCCAT CGATGTGGTG 120

GTATCTAGGG GATCGCCAGC AACCCTCAAC TGTGGTGCAA AGCCATCTAC CGCCAAAATC 180

ACATGGTACA AGGATGGACA GCCCGTAATC ACGAATAAGG AGCAAGTGAA CAGCCACCGG 240
ATTGTTCTCG ACACGGGATC CCTGTTTCTT CTGAAAGTGA ATAGTGGAAA AAACGGAAAA 300
GACAGCGATG CGGGAGCGTA CTATTGTGTG GCCAGCAACG AGCACGGAGA AGTGAAGTCG 360
AACGAAGGAT CGTTAAAATT GGCGATGCTT CGCGAAGACT TTCGAGTTCG GCCAAGAACA 420
GTTCAGGCTC TTGGTGGAGA GATGGCCGTT CTGGAATGCA GTCCGCCACG TGGATTCCCG 480
GAGCCGGTTG TGAGCTGGCG GAAAGACGAC AAAGAGCTCC GAATTCAAGA CATGCCACGA 540
TACACTCTAC ACTCTGACGG AAACCTCATC ATTGATCCGG TCGATCGAAG CGATTCTGGT 600
ACTTATCAGT GTGTTGCCAA CAACATGGTC GGAGAACGGG TGTCCAATCC CGCAAGATTG 660
AGTGTCTTTG AGAAACCAAA GTTTGAGCAA GAACCCAAGG ACATGACGGT CGACGTCGGA 720
GCCGCAGTGC TGTTTGATTG TCGTGTGACT GGAGATCCTC AACCACAAAT TACGTGGAAA 780
CGCAAAAATG AGCCGATGCC AGTTACACGT GCATACATTG CCAAGGATAA TCGGGGGTTG 840
AGAATCGAAA GAGTTCAACC ATCAGACGAA GGTGAATACG TTTGCTATGC ACGAAATCCA 900
GCGGGAACTC TTGAAGCATC TGCACATCTT CGTGTCCAGG CACCTCCATC CTTCCAGACA 960
AAACCAGCAG ACCAGTCAGT TCCAGCTGGA GGCACGGCAA CTTTTGAATG CACCTTGGTC 1020
GGTCAACCGA GTCCCGCCTA TTTTTGGAGC AAGGAAGGCC AACAGGATCT TCTTTTCCCA 1080
AGTTATGTGT CCGCTGATGG TAGAACGAAA GTTTCACCAA CTGGAACATT GACAATTGAG 1140
GAAGTTCGTC AAGTTGATGA GGGAGCTTAT GTGTGCGCTG GAATGAACTC GGCAGGAAGC 1200
TCGTTGAGCA AGGCAGCTTT GAAAGCAACA TTTGAAACCA AAGGCCGTGT CCAAAAAAAA 1260
AAGAGCAAAA TGGGCAAACA GAAACAAAAA AATGTTCAAT CAATTATCAA ATATTTAATT 1320
TCAGCCGTGA CCGGAAACAC ACCCGCCAAA CCACCACCAA CAATCGAGCA TGGTCATCAA 1380
AATCAGACCC TTATGGTTGG ATCATCAGCC ATCCTTCCAT GTCAGGCTAG CGGAAAACCA 1440
ACTCCAGGAA TATCATGGCT CAGGGATGGG CTACCTATTG ACATTACAGA TAGTCGTATC 1500
AGTCAACATT CAACGGGAAG TCTACATATT GCCGATTTAA AGAAACCTGA CACCGGAGTT 1560
TACACTTGCA TTGCGAAGAA CGAGGATGGA GAGTCAACAT GGTCGGCATC TCTGACTGTT 1620
GAAGATCACA CTAGCAATGC ACAATTTGTT CGGATGCCGG ATCCATCGAA CTTCCCGTCT 1680
TCTCCAACGC AACCCATTAT TGTCAATGTC ACTGATACCG AAGTAGAGCT CCACTGGAAT 1740
GCTCCCTCCA CATCTGGCGC AGGACCAATC ACTGGTTATA TCATTCAGTA CTACAGTCCA 1800
GACCTCGGAC AGACGTGGTT TAACATTCCA GACTACGTGG CATCTACTGA ATATAGAATA 1860
AAGGGTCTGA AACCATCTCA CTCGTATATG TTTGTGATTC GAGCAGAAAA TGAGAAAGGT 1920
ATTGGAACGC CGAGTGTGTC GTCGGCTCTC GTTACCACTA GCAAGCCAGC AGCTCAAGTT 1980
GCGCTTTCTG ACAAGAACAA AATGGACATG GCCATCGCTG AGAAGAGACT CACTTCGGAA 2040
CAACTCATAA AACTCGAGGA AGTGAAGACT ATTAATTCTA CGGCCGTTCG TTTGTTCTGG 2100
AAGAAGAGGA AACTTGAAGA GCTGATTGAT GGTTACTACA TCAAGTGGAG AGGGCCTCCA 2160
AGAACCAATG ATAATCAATA CGTGAATGTG ACCAGCCCTA GCACCGAAAA CTATGTTGTT 2220
TCAAATTTAA TGCCATTCAC CAACTATGAG TTTTTCGTGA TTCCTTATCA TTCCGGAGTT 2280
CATAGTATTC ATGGAGCACC GAGTAATTCC ATGGACGTGT TGACCGCCGA AGCTCCACCT 2340
TCATTGCCAC CAGAGGATGT GCGAATCCGT ATGCTCAACC TGACCACTCT TCGTATCTCT 2400
TGGAAAGCAC CAAAAGCCGA CGGCATCAAC GGAATTCTCA AAGGATTCCA AATTGTTATT 2460

GTTGGTCAAG CGCCCAACAA CAATCGGAAC ATCACTACAA ACGAGAGAGC TGCCAGTGTT 2520
ACTCTGTTCC ATTTAGTGAC TGGAATGACG TATAAAATTC GTGTAGCGGC TAGAAGCAAT 2580
GGTGGAGTTG GAGTCTCACA TGGAACGAGT GAAGTCATCA TGAATCAAGA CACGCTGGAA 2640
AAACACCTTG CTGCTCAACA AGAAAACGAA TCATTTTTGT ATGGGCTGAT CAATAAATCT 2700
CATGTTCCTG TGATTGTCAT TGTTGCAATT CTGATTATTT TCGTAGTCAT CATTATAGCC 2760
TATTGTTACT GGAGGAATAG CAGAAACAGT GATGGAAAGG ATCGAAGTTT TATAAAGATC 2820
AATGATGGAA GTGTTCATAT GGCTTCGAAT AATCTTTGGG ATGTTGCACA AAATCCGAAT 2880
CAGAATCCAA TGTACAACAC TGCTGGAAGA ATGACTATGA ACAATAGAAA TGGCCAGGCT 2940
CTCTATTCGC TGACACCAAA TGCGCAAGAC TTTTTCAACA ATTGTGATGA CTACAGTGGA 3000
ACGATGCACA GACCAGGATC CGAGCATCAC TATCATTATG CTCAACTGAC TGGCGGACCT 3060
GGTAATGCGA TGTCTACTTT TTATGGAAAC CAATATCACG ATGATCCATC TCCATATGCC 3120
ACCACAACAC TGGTCCTGTC GAACCAACAA CCAGCTTGGC TCAATGACAA AATGCTTCGC 3180
GCGCCAGCAA TGCCAACAAA TCCCGTGCCA CCAGAGCCAC CGGCGCGATA TGCAGATCAT 3240
ACCGCTGGAA GACGATCTCG ATCGAGCCGT GCATCCGATG GGAGAGGAAC TCTGAATGGC 3300
GGACTCCATC ACCGGACTAG CGGAAGTCAA CGGTCGGATA GTCCACCTCA CACAGATGTG 3360
AGCTATGTTC AGCTTCACTC ATCCGATGGA ACTGGTAGTA GTAAGGAAAG AACTGGGGAG 3420
CGGAGAACAC CACCGAATAA GACTCTGATG GACTTTATTC CGCCACCACC TTCCAATCCA 3480
CCACCACCTG GAGGGCACGT TTATGACACA GCAACTAGGC GTCAGTTGAA TCGTGGAAGT 3540
ACTCCACGAG AAGACACCTA CGATTCGGTC AGTGACGGAG CTTTTGCTCG GGTTGATGTG 3600
AATGCAAGGC CAACGAGTCG GAATCGGAAT TTGGGAGGAA GGCCGCTGAA AGGGAAACGA 3660
GACGACGATA GTCAGCGGTC TTCGTTGATG ATGGACGATG ATGGTGGATC TTCTGAAGCT 3720
GACGGGGAGA ACTCTGAAGG AGACGTTCCG CGTGGAGGTG TTAGAAAAGC AGTTCCTCGA 3780
ATGGGTATCT CTGCAAGTAC GCTGGCTCAT AGTTGTTACG GGACAAACGG CACTGCTCAA 3840
CGATTCCGGT CAATTCCACG TAACAATGGA ATCGTCACAC AAGAACAAAC TTGA 3894

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Tyr Tyr Leu Gly Phe Tyr His Thr His Thr His Thr His Thr Tyr
1 5 10 15

Ile Asn Phe Asp Lys Ile Pro Asn Ala Ser Asn Leu Ala Pro Val Ile
20 25 30

Ile Glu His Pro Ile Asp Val Val Val Ser Arg Gly Ser Pro Ala Thr

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         35                  40                  45
Leu Asn Cys Gly Ala Lys Pro Ser Thr Ala Lys Ile Thr Trp Tyr Lys
     50                  55                  60
Asp Gly Gln Pro Val Ile Thr Asn Lys Glu Gln Val Asn Ser His Arg
65                   70                  75                  80
Ile Val Leu Asp Thr Gly Ser Leu Phe Leu Leu Lys Val Asn Ser Gly
                 85                  90                  95
Lys Asn Gly Lys Asp Ser Asp Ala Gly Ala Tyr Tyr Cys Val Ala Ser
            100                 105                 110
Asn Glu His Gly Glu Val Lys Ser Asn Glu Gly Ser Leu Lys Leu Ala
        115                 120                 125
Met Leu Arg Glu Asp Phe Arg Val Arg Pro Arg Thr Val Gln Ala Leu
    130                 135                 140
Gly Gly Glu Met Ala Val Leu Glu Cys Ser Pro Pro Arg Gly Phe Pro
145                 150                 155                 160
Glu Pro Val Val Ser Trp Arg Lys Asp Asp Lys Glu Leu Arg Ile Gln
                165                 170                 175
Asp Met Pro Arg Tyr Thr Leu His Ser Asp Gly Asn Leu Ile Ile Asp
            180                 185                 190
Pro Val Asp Arg Ser Asp Ser Gly Thr Tyr Gln Cys Val Ala Asn Asn
        195                 200                 205
Met Val Gly Glu Arg Val Ser Asn Pro Ala Arg Leu Ser Val Phe Glu
    210                 215                 220
Lys Pro Lys Phe Glu Gln Glu Pro Lys Asp Met Thr Val Asp Val Gly
225                 230                 235                 240
Ala Ala Val Leu Phe Asp Cys Arg Val Thr Gly Asp Pro Gln Pro Gln
                245                 250                 255
Ile Thr Trp Lys Arg Lys Asn Glu Pro Met Pro Val Thr Arg Ala Tyr
            260                 265                 270
Ile Ala Lys Asp Asn Arg Gly Leu Arg Ile Glu Arg Val Gln Pro Ser
        275                 280                 285
Asp Glu Gly Glu Tyr Val Cys Tyr Ala Arg Asn Pro Ala Gly Thr Leu
    290                 295                 300
Glu Ala Ser Ala His Leu Arg Val Gln Ala Pro Pro Ser Phe Gln Thr
305                 310                 315                 320
Lys Pro Ala Asp Gln Ser Val Pro Ala Gly Gly Thr Ala Thr Phe Glu
                325                 330                 335
Cys Thr Leu Val Gly Gln Pro Ser Pro Ala Tyr Phe Trp Ser Lys Glu
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                340                 345                 350
Gly Gln Gln Asp Leu Leu Phe Pro Ser Tyr Val Ser Ala Asp Gly Arg
        355                 360                 365
Thr Lys Val Ser Pro Thr Gly Thr Leu Thr Ile Glu Glu Val Arg Gln
    370                 375                 380
Val Asp Glu Gly Ala Tyr Val Cys Ala Gly Met Asn Ser Ala Gly Ser
385                 390                 395                 400
Ser Leu Ser Lys Ala Ala Leu Lys Ala Thr Phe Glu Thr Lys Gly Arg
                405                 410                 415
Val Gln Lys Lys Lys Ser Lys Met Gly Lys Gln Lys Gln Lys Asn Val
            420                 425                 430
Gln Ser Ile Ile Lys Tyr Leu Ile Ser Ala Val Thr Gly Asn Thr Pro
        435                 440                 445
Ala Lys Pro Pro Pro Thr Ile Glu His Gly His Gln Asn Gln Thr Leu
    450                 455                 460
Met Val Gly Ser Ser Ala Ile Leu Pro Cys Gln Ala Ser Gly Lys Pro
465                 470                 475                 480
Thr Pro Gly Ile Ser Trp Leu Arg Asp Gly Leu Pro Ile Asp Ile Thr
                485                 490                 495
Asp Ser Arg Ile Ser Gln His Ser Thr Gly Ser Leu His Ile Ala Asp
            500                 505                 510
Leu Lys Lys Pro Asp Thr Gly Val Tyr Thr Cys Ile Ala Lys Asn Glu
        515                 520                 525
Asp Gly Glu Ser Thr Trp Ser Ala Ser Leu Thr Val Glu Asp His Thr
    530                 535                 540
Ser Asn Ala Gln Phe Val Arg Met Pro Asp Pro Ser Asn Phe Pro Ser
545                 550                 555                 560
Ser Pro Thr Gln Pro Ile Ile Val Asn Val Thr Asp Thr Glu Val Glu
                565                 570                 575
Leu His Trp Asn Ala Pro Ser Thr Ser Gly Ala Gly Pro Ile Thr Gly
            580                 585                 590
Tyr Ile Ile Gln Tyr Tyr Ser Pro Asp Leu Gly Gln Thr Trp Phe Asn
        595                 600                 605
Ile Pro Asp Tyr Val Ala Ser Thr Glu Tyr Arg Ile Lys Gly Leu Lys
    610                 615                 620
Pro Ser His Ser Tyr Met Phe Val Ile Arg Ala Glu Asn Glu Lys Gly
625                 630                 635                 640
Ile Gly Thr Pro Ser Val Ser Ser Ala Leu Val Thr Thr Ser Lys Pro
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645 650 655

Ala Ala Gln Val Ala Leu Ser Asp Lys Asn Lys Met Asp Met Ala Ile

660 665 670

Ala Glu Lys Arg Leu Thr Ser Glu Gln Leu Ile Lys Leu Glu Glu Val

675 680 685

Lys Thr Ile Asn Ser Thr Ala Val Arg Leu Phe Trp Lys Lys Arg Lys

690 695 700

Leu Glu Glu Leu Ile Asp Gly Tyr Tyr Ile Lys Trp Arg Gly Pro Pro

705 710 715 720

Arg Thr Asn Asp Asn Gln Tyr Val Asn Val Thr Ser Pro Ser Thr Glu

725 730 735

Asn Tyr Val Val Ser Asn Leu Met Pro Phe Thr Asn Tyr Glu Phe Phe

740 745 750

Val Ile Pro Tyr His Ser Gly Val His Ser Ile His Gly Ala Pro Ser

755 760 765

Asn Ser Met Asp Val Leu Thr Ala Glu Ala Pro Pro Ser Leu Pro Pro

770 775 780

Glu Asp Val Arg Ile Arg Met Leu Asn Leu Thr Thr Leu Arg Ile Ser

785 790 795 800

Trp Lys Ala Pro Lys Ala Asp Gly Ile Asn Gly Ile Leu Lys Gly Phe

805 810 815

Gln Ile Val Ile Val Gly Gln Ala Pro Asn Asn Asn Arg Asn Ile Thr

820 825 830

Thr Asn Glu Arg Ala Ala Ser Val Thr Leu Phe His Leu Val Thr Gly

835 840 845

Met Thr Tyr Lys Ile Arg Val Ala Ala Arg Ser Asn Gly Gly Val Gly

850 855 860

Val Ser His Gly Thr Ser Glu Val Ile Met Asn Gln Asp Thr Leu Glu

865 870 875 880

Lys His Leu Ala Ala Gln Gln Glu Asn Glu Ser Phe Leu Tyr Gly Leu

885 890 895

Ile Asn Lys Ser His Val Pro Val Ile Val Ile Val Ala Ile Leu Ile

900 905 910

Ile Phe Val Val Ile Ile Ile Ala Tyr Cys Tyr Trp Arg Asn Ser Arg

915 920 925

Asn Ser Asp Gly Lys Asp Arg Ser Phe Ile Lys Ile Asn Asp Gly Ser

930 935 940

Val His Met Ala Ser Asn Asn Leu Trp Asp Val Ala Gln Asn Pro Asn

945 950 955 960

Gln Asn Pro Met Tyr Asn Thr Ala Gly Arg Met Thr Met Asn Asn Arg
965 970 975

Asn Gly Gln Ala Leu Tyr Ser Leu Thr Pro Asn Ala Gln Asp Phe Phe
980 985 990

Asn Asn Cys Asp Asp Tyr Ser Gly Thr Met His Arg Pro Gly Ser Glu
995 1000 1005

His His Tyr His Tyr Ala Gln Leu Thr Gly Gly Pro Gly Asn Ala Met
1010 1015 1020

Ser Thr Phe Tyr Gly Asn Gln Tyr His Asp Asp Pro Ser Pro Tyr Ala
1025 1030 1035 1040

Thr Thr Thr Leu Val Leu Ser Asn Gln Gln Pro Ala Trp Leu Asn Asp
1045 1050 1055

Lys Met Leu Arg Ala Pro Ala Met Pro Thr Asn Pro Val Pro Pro Glu
1060 1065 1070

Pro Pro Ala Arg Tyr Ala Asp His Thr Ala Gly Arg Arg Ser Arg Ser
1075 1080 1085

Ser Arg Ala Ser Asp Gly Arg Gly Thr Leu Asn Gly Gly Leu His His
1090 1095 1100

Arg Thr Ser Gly Ser Gln Arg Ser Asp Ser Pro Pro His Thr Asp Val
1105 1110 1115 1120

Ser Tyr Val Gln Leu His Ser Ser Asp Gly Thr Gly Ser Ser Lys Glu
1125 1130 1135

Arg Thr Gly Glu Arg Arg Thr Pro Pro Asn Lys Thr Leu Met Asp Phe
1140 1145 1150

Ile Pro Pro Pro Pro Ser Asn Pro Pro Pro Pro Gly Gly His Val Tyr
1155 1160 1165

Asp Thr Ala Thr Arg Arg Gln Leu Asn Arg Gly Ser Thr Pro Arg Glu
1170 1175 1180

Asp Thr Tyr Asp Ser Val Ser Asp Gly Ala Phe Ala Arg Val Asp Val
1185 1190 1195 1200

Asn Ala Arg Pro Thr Ser Arg Asn Arg Asn Leu Gly Gly Arg Pro Leu
1205 1210 1215

Lys Gly Lys Arg Asp Asp Asp Ser Gln Arg Ser Ser Leu Met Met Asp
1220 1225 1230

Asp Asp Gly Gly Ser Ser Glu Ala Asp Gly Glu Asn Ser Glu Gly Asp
1235 1240 1245

Val Pro Arg Gly Gly Val Arg Lys Ala Val Pro Arg Met Gly Ile Ser

1250 1255 1260

Ala Ser Thr Leu Ala His Ser Cys Tyr Gly Thr Asn Gly Thr Ala Gln

1265 1270 1275 1280

Arg Phe Arg Ser Ile Pro Arg Asn Asn Gly Ile Val Thr Gln Glu Gln

1285 1290 1295

Thr

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4956 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAAATGGA AACATGTTCC TTTTTTGGTC ATGATATCAC TCCTCAGCTT ATCCCCAAAT 60

CACCTGTTTC TGGCCCAGCT TATTCCAGAC CCTGAAGATG TAGAGAGGGG GAACGACCAC 120

GGGACGCCAA TCCCCACCTC TGATAACGAT GACAATTCGC TGGGCTATAC AGGCTCCCGT 180

CTTCGTCAGG AAGATTTTCC ACCTCGCATT GTTGAACACC CTTCAGACCT GATTGTCTCA 240

AAAGGAGAAC CTGCAACTTT GAACTGCAAA GCTGAAGGCC GCCCCACACC CACTATTGAA 300

TGGTACAAAG GGGGAGAGAG AGTGGAGACA GACAAAGATG ACCCTCGCTC ACACCGAATG 360

TTGCTGCCGA GTGGATCTTT ATTTTTCTTA CGTATAGTAC ATGGACGGAA AAGTAGACCT 420

GATGAAGGAG TCTATGTCTG TGTAGCAAGG AATTACCTTG GAGAGGCTGT GAGCCACAAT 480

GCATCGCTGG AAGTAGCCAT ACTTCGGGAT GACTTCAGAC AAAACCCTTC GGATGTCATG 540

GTTGCAGTAG GAGAGCCTGC AGTAATGGAA TGCCAACCTC CACGAGGCCA TCCTGAGCCC 600

ACCATTTCAT GGAAGAAAGA TGGCTCTCCA CTGGATGATA AAGATGAAAG AATAACTATA 660

CGAGGAGGAA AGCTCATGAT CACTTACACC CGTAAAAGTG ACGCTGGCAA ATATGTTTGT 720

GTTGGTACCA ATATGGTTGG GGAACGTGAG AGTGAAGTAG CCGAGCTGAC TGTCTTAGAG 780

AGACCATCAT TTGTGAAGAG ACCCAGTAAC TTGGCAGTAA CTGTGGATGA CAGTGCAGAA 840

TTTAAATGTG AGGCCCGAGG TGACCCTGTA CCTACAGTAC GATGGAGGAA AGATGATGGA 900

GAGCTGCCCA AATCCAGATA TGAAATCCGA GATGATCATA CCTTGAAAAT TAGGAAGGTG 960

ACAGCTGGTG ACATGGGTTC ATACACTTGT GTTGCAGAAA ATATGGTGGG CAAAGCTGAA 1020

GCATCTGCTA CTCTGACTGT TCAAGAACCT CCACATTTTG TTGTGAAACC CCGTGACCAG 1080

GTTGTTGCTT TGGGACGGAC TGTAACTTTT CAGTGTGAAG CAACCGGAAA TCCTCAACCA 1140

GCTATTTTCT GGAGGAGAGA AGGGAGTCAG AATCTACTTT TCTCATATCA ACCACCACAG 1200

TCATCCAGCC GATTTTCAGT CTCCCAGACT GGCGACCTCA CAATTACTAA TGTCCAGCGA 1260

TCTGATGTTG GTTATTACAT CTGCCAGACT TTAAATGTTG CTGGAAGCAT CATCACAAAG 1320

GCATATTTGG AAGTTACAGA TGTGATTGCA GATCGGCCTC CCCCAGTTAT TCGACAAGGT 1380

CCTGTGAATC AGACTGTAGC CGTGGATGGC ACTTTCGTCC TCAGCTGTGT GGCCACAGGC 1440

AGTCCAGTGC CCACCATTCT GTGGAGAAAG GATGGAGTCC TCGTTTCAAC CCAAGACTCT 1500

CGAATCAAAC AGTTGGAGAA TGGAGTACTG CAGATCCGAT ATGCTAAGCT GGGTGATACT 1560

GGTCGGTACA CCTGCATTGC ATCAACCCCC AGTGGTGAAG CAACATGGAG TGCTTACATT 1620

GAAGTTCAAG AATTTGGAGT TCCAGTTCAG CCTCCAAGAC CTACTGACCC AAATTTAATC 1680

CCTAGTGCCC CATCAAAACC TGAAGTGACA GATGTCAGCA GAAATACAGT CACATTATCG 1740

TGGCAACCAA ATTTGAATTC AGGAGCAACT CCAACATCTT ATATTATAGA AGCCTTCAGC 1800

CATGCATCTG GTAGCAGCTG GCAGACCGTA GCAGAGAATG TGAAAACAGA AACATCTGCC 1860

ATTAAAGGAC TCAAACCTAA TGCAATTTAC CTTTTCCTTG TGAGGGCAGC TAATGCATAT 1920

GGAATTAGTG ATCCAAGCCA AATATCAGAT CCAGTGAAAA CACAAGATGT CCTACCAACA 1980

AGTCAGGGGG TGGACCACAA GCAGGTCCAG AGAGAGCTGG GAAATGCTGT TCTGCACCTC 2040

CACAACCCCA CCGTCCTTTC TTCCTCTTCC ATCGAAGTGC ACTGGACAGT AGATCAACAG 2100

TCTCAGTATA TACAAGGATA TAAAATTCTC TATCGGCCAT CTGGAGCCAA CCACGGAGAA 2160

TCAGACTGGT TAGTTTTTGA AGTGAGGACG CCAGCCAAAA ACAGTGTGGT AATCCCTGAT 2220

CTCAGAAAGG GAGTCAACTA TGAAATTAAG GCTCGCCCTT TTTTTAATGA ATTTCAAGGA 2280

GCAGATAGTG AAATCAAGTT TGCCAAAACC CTGGAAGAAG CACCCAGTGC CCCACCCCAA 2340

GGTGTAACTG TATCCAAGAA TGATGGAAAC GGAACTGCAA TTCTAGTTAG TTGGCAGCCA 2400

CCTCCAGAAG ACACTCAAAA TGGAATGGTC CAAGAGTATA AGGTTTGGTG TCTGGGCAAT 2460

GAAACTCGAT ACCACATCAA CAAAACAGTG GATGGTTCCA CCTTTTCCGT GGTCATTCCC 2520

TTTCTTGTTC CTGGAATCCG ATACAGTGTG GAAGTGGCAG CCAGCACTGG GGCTGGGTCT 2580

GGGGTAAAGA GTGAGCCTCA GTTCATCCAG CTGGATGCCC ATGGAAACCC TGTGTCACCT 2640

GAGGACCAAG TCAGCCTCGC TCAGCAGATT TCAGATGTGG TGAAGCAGCC GGCCTTCATA 2700

GCAGGTATTG GAGCAGCCTG TTGGATCATC CTCATGGTCT TCAGCATCTG GCTTTATCGA 2760

CACCGCAAGA AGAGAAACGG ACTTACTAGT ACCTACGCGG GTATCAGAAA AGTCCCGTCT 2820

TTTACCTTCA CACCAACAGT AACTTACCAG AGAGGAGGCG AAGCTGTCAG CAGTGGAGGG 2880

AGGCCTGGAC TTCTCAACAT CAGTGAACCT GCCGCGCAGC CATGGCTGGC AGACACGTGG 2940

CCTAATACTG GCAACAACCA CAATGACTGC TCCATCAGCT GCTGCACGGC AGGCAATGGA 3000

AACAGCGACA GCAACCTCAC TACCTACAGT CGCCCAGCTG ATTGTATAGC AAATTATAAC 3060

AACCAACTGG ATAACAAACA AACAAATCTG ATGCTCCCTG AGTCAACTGT TTATGGTGAT 3120

GTGGACCTTA GTAACAAAAT CAATGAGATG AAAACCTTCA ATAGCCCAAA TCTGAAGGAT 3180

GGGCGTTTTG TCAATCCATC AGGGCAGCCT ACTCCTTACG CCACCACTCA GCTCATCCAG 3240

TCAAACCTCA GCAACAACAT GAACAATGGC AGCGGGGACT CTGGCGAGAA GCACTGGAAA 3300

CCACTGGGAC AGCAGAAACA AGAAGTGGCA CCAGTTCAGT ACAACATCGT GGAGCAAAAC 3360

AAGCTGAACA AAGATTATCG AGCAAATGAC ACAGTTCCTC CAACTATCCC ATACAACCAA 3420

TCATACGACC AGAACACAGG AGGATCCTAC AACAGCTCAG ACCGGGGCAG TAGTACATCT 3480

GGGAGTCAGG GGCACAAGAA AGGGGCAAGA ACACCCAAGG TACCAAAACA GGGTGGCATG 3540

AACTGGGCAG ACCTGCTTCC TCCTCCCCCA GCACATCCTC CTCCACACAG CAATAGCGAA 3600

GAGTACAACA TTTCTGTAGA TGAAAGCTAT GACCAAGAAA TGCCATGTCC CGTGCCACCA 3660

GCAAGGATGT ATTTGCAACA AGATGAATTA GAAGAGGAGG AAGATGAACG AGGCCCCACT 3720

CCCCCTGTTC GGGGAGCAGC TTCTTCTCCA GCTGCCGTGT CCTATAGCCA TCAGTCCACT 3780

GCCACTCTGA CTCCCTCCCC ACAGGAAGAA CTCCAGCCCA TGTTACAGGA TTGTCCAGAG 3840

GAGACTGGCC ACATGCAGCA CCAGCCCGAC AGGAGACGGC AGCCTGTGAG TCCTCCTCCA 3900

CCACCACGGC CGATCTCCCC TCCACATACC TATGGCTACA TTTCAGGACC CCTGGTCTCA 3960

GATATGGATA CGGATGCGCC AGAAGAGGAA GAAGACGAAG CCGACATGGA GGTAGCCAAG 4020

ATGCAAACCA GAAGGCTTTT GTTACGTGGG CTTGAGCAGA CACCTGCCTC CAGTGTTGGG 4080

GACCTGGAGA GCTCTGTCAC GGGGTCCATG ATCAACGGCT GGGGCTCAGC CTCAGAGGAG 4140

GACAACATTT CCAGCGGACG CTCCAGTGTT AGTTCTTCGG ACGGCTCCTT TTTCACTGAT 4200

GCTGACTTTG CCCAGGCAGT CGCAGCAGCG GCAGAGTATG CTGGTCTGAA AGTAGCACGA 4260

CGGCAAATGC AGGATGCTGC TGGCCGTCGA CATTTTCATG CGTCTCAGTG CCCTAGGCCC 4320

ACAAGTCCCG TGTCTACAGA CAGCAACATG AGTGCCGCCG TAATGCAGAA AACCAGACCA 4380

GCCAAGAAAC TGAAACACCA GCCAGGACAT CTGCGCAGAG AAACCTACAC AGATGATCTT 4440

CCACCACCTC CTGTGCCGCC ACCTGCTATA AAGTCACCTA CTGCCCAATC CAAGACACAG 4500

CTGGAAGTAC GACCTGTAGT GGTGCCAAAA CTCCCTTCTA TGGATGCAAG AACAGACAGA 4560

TCATCAGACA GAAAAGGAAG CAGTTACAAG GGGAGAGAAG TGTTGGATGG AAGACAGGTT 4620

GTTGACATGC GAACAAATCC AGGTGATCCC AGAGAAGCAC AGGAACAGCA AAATGACGGG 4680

AAAGGACGTG GAAACAAGGC AGCAAAACGA GACCTTCCAC CAGCAAAGAC TCATCTCATC 4740

CAAGAGGATA TTCTACCTTA TTGTAGACCT ACTTTTCCAA CATCAAATAA TCCCAGAGAT 4800

CCCAGTTCCT CAAGCTCAAT GTCATCAAGA GGATCAGGAA GCAGACAAAG AGAACAAGCA 4860

AATGTAGGTC GAAGAAATAT TGCAGAAATG CAGGTACTTG GAGGATATGA AAGAGGAGAA 4920

GATAATAATG AAGAATTAGA GGAAACTGAA AGCTGA 4956

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1651 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Lys Trp Lys His Val Pro Phe Leu Val Met Ile Ser Leu Leu Ser
1 5 10 15

Leu Ser Pro Asn His Leu Phe Leu Ala Gln Leu Ile Pro Asp Pro Glu
20 25 30

Asp Val Glu Arg Gly Asn Asp His Gly Thr Pro Ile Pro Thr Ser Asp
35 40 45

Asn Asp Asp Asn Ser Leu Gly Tyr Thr Gly Ser Arg Leu Arg Gln Glu

50 55 60

Asp Phe Pro Pro Arg Ile Val Glu His Pro Ser Asp Leu Ile Val Ser
65 70 75 80

Lys Gly Glu Pro Ala Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr
85 90 95

Pro Thr Ile Glu Trp Tyr Lys Gly Gly Glu Arg Val Glu Thr Asp Lys
100 105 110

Asp Asp Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe
115 120 125

Phe Leu Arg Ile Val His Gly Arg Lys Ser Arg Pro Asp Glu Gly Val
130 135 140

Tyr Val Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser His Asn
145 150 155 160

Ala Ser Leu Glu Val Ala Ile Leu Arg Asp Asp Phe Arg Gln Asn Pro
165 170 175

Ser Asp Val Met Val Ala Val Gly Glu Pro Ala Val Met Glu Cys Gln
180 185 190

Pro Pro Arg Gly His Pro Glu Pro Thr Ile Ser Trp Lys Lys Asp Gly
195 200 205

Ser Pro Leu Asp Asp Lys Asp Glu Arg Ile Thr Ile Arg Gly Gly Lys
210 215 220

Leu Met Ile Thr Tyr Thr Arg Lys Ser Asp Ala Gly Lys Tyr Val Cys
225 230 235 240

Val Gly Thr Asn Met Val Gly Glu Arg Glu Ser Glu Val Ala Glu Leu
245 250 255

Thr Val Leu Glu Arg Pro Ser Phe Val Lys Arg Pro Ser Asn Leu Ala
260 265 270

Val Thr Val Asp Asp Ser Ala Glu Phe Lys Cys Glu Ala Arg Gly Asp
275 280 285

Pro Val Pro Thr Val Arg Trp Arg Lys Asp Asp Gly Glu Leu Pro Lys
290 295 300

Ser Arg Tyr Glu Ile Arg Asp Asp His Thr Leu Lys Ile Arg Lys Val
305 310 315 320

Thr Ala Gly Asp Met Gly Ser Tyr Thr Cys Val Ala Glu Asn Met Val
325 330 335

Gly Lys Ala Glu Ala Ser Ala Thr Leu Thr Val Gln Glu Pro Pro His
340 345 350

Phe Val Val Lys Pro Arg Asp Gln Val Val Ala Leu Gly Arg Thr Val

```
         355                 360                 365
Thr Phe Gln Cys Glu Ala Thr Gly Asn Pro Gln Pro Ala Ile Phe Trp
    370                 375                 380
Arg Arg Glu Gly Ser Gln Asn Leu Leu Phe Ser Tyr Gln Pro Pro Gln
385                 390                 395                 400
Ser Ser Ser Arg Phe Ser Val Ser Gln Thr Gly Asp Leu Thr Ile Thr
                405                 410                 415
Asn Val Gln Arg Ser Asp Val Gly Tyr Tyr Ile Cys Gln Thr Leu Asn
            420                 425                 430
Val Ala Gly Ser Ile Ile Thr Lys Ala Tyr Leu Glu Val Thr Asp Val
        435                 440                 445
Ile Ala Asp Arg Pro Pro Pro Val Ile Arg Gln Gly Pro Val Asn Gln
    450                 455                 460
Thr Val Ala Val Asp Gly Thr Phe Val Leu Ser Cys Val Ala Thr Gly
465                 470                 475                 480
Ser Pro Val Pro Thr Ile Leu Trp Arg Lys Asp Gly Val Leu Val Ser
                485                 490                 495
Thr Gln Asp Ser Arg Ile Lys Gln Leu Glu Asn Gly Val Leu Gln Ile
            500                 505                 510
Arg Tyr Ala Lys Leu Gly Asp Thr Gly Arg Tyr Thr Cys Ile Ala Ser
        515                 520                 525
Thr Pro Ser Gly Glu Ala Thr Trp Ser Ala Tyr Ile Glu Val Gln Glu
    530                 535                 540
Phe Gly Val Pro Val Gln Pro Pro Arg Pro Thr Asp Pro Asn Leu Ile
545                 550                 555                 560
Pro Ser Ala Pro Ser Lys Pro Glu Val Thr Asp Val Ser Arg Asn Thr
                565                 570                 575
Val Thr Leu Ser Trp Gln Pro Asn Leu Asn Ser Gly Ala Thr Pro Thr
            580                 585                 590
Ser Tyr Ile Ile Glu Ala Phe Ser His Ala Ser Gly Ser Ser Trp Gln
        595                 600                 605
Thr Val Ala Glu Asn Val Lys Thr Glu Thr Ser Ala Ile Lys Gly Leu
    610                 615                 620
Lys Pro Asn Ala Ile Tyr Leu Phe Leu Val Arg Ala Ala Asn Ala Tyr
625                 630                 635                 640
Gly Ile Ser Asp Pro Ser Gln Ile Ser Asp Pro Val Lys Thr Gln Asp
                645                 650                 655
Val Leu Pro Thr Ser Gln Gly Val Asp His Lys Gln Val Gln Arg Glu
```

660 665 670

Leu Gly Asn Ala Val Leu His Leu His Asn Pro Thr Val Leu Ser Ser

675 680 685

Ser Ser Ile Glu Val His Trp Thr Val Asp Gln Gln Ser Gln Tyr Ile

690 695 700

Gln Gly Tyr Lys Ile Leu Tyr Arg Pro Ser Gly Ala Asn His Gly Glu

705 710 715 720

Ser Asp Trp Leu Val Phe Glu Val Arg Thr Pro Ala Lys Asn Ser Val

725 730 735

Val Ile Pro Asp Leu Arg Lys Gly Val Asn Tyr Glu Ile Lys Ala Arg

740 745 750

Pro Phe Phe Asn Glu Phe Gln Gly Ala Asp Ser Glu Ile Lys Phe Ala

755 760 765

Lys Thr Leu Glu Glu Ala Pro Ser Ala Pro Pro Gln Gly Val Thr Val

770 775 780

Ser Lys Asn Asp Gly Asn Gly Thr Ala Ile Leu Val Ser Trp Gln Pro

785 790 795 800

Pro Pro Glu Asp Thr Gln Asn Gly Met Val Gln Glu Tyr Lys Val Trp

805 810 815

Cys Leu Gly Asn Glu Thr Arg Tyr His Ile Asn Lys Thr Val Asp Gly

820 825 830

Ser Thr Phe Ser Val Val Ile Pro Phe Leu Val Pro Gly Ile Arg Tyr

835 840 845

Ser Val Glu Val Ala Ala Ser Thr Gly Ala Gly Ser Gly Val Lys Ser

850 855 860

Glu Pro Gln Phe Ile Gln Leu Asp Ala His Gly Asn Pro Val Ser Pro

865 870 875 880

Glu Asp Gln Val Ser Leu Ala Gln Gln Ile Ser Asp Val Val Lys Gln

885 890 895

Pro Ala Phe Ile Ala Gly Ile Gly Ala Ala Cys Trp Ile Ile Leu Met

900 905 910

Val Phe Ser Ile Trp Leu Tyr Arg His Arg Lys Lys Arg Asn Gly Leu

915 920 925

Thr Ser Thr Tyr Ala Gly Ile Arg Lys Val Pro Ser Phe Thr Phe Thr

930 935 940

Pro Thr Val Thr Tyr Gln Arg Gly Gly Glu Ala Val Ser Ser Gly Gly

945 950 955 960

Arg Pro Gly Leu Leu Asn Ile Ser Glu Pro Ala Ala Gln Pro Trp Leu

965 970 975

Ala Asp Thr Trp Pro Asn Thr Gly Asn Asn His Asn Asp Cys Ser Ile

980 985 990

Ser Cys Cys Thr Ala Gly Asn Gly Asn Ser Asp Ser Asn Leu Thr Thr

995 1000 1005

Tyr Ser Arg Pro Ala Asp Cys Ile Ala Asn Tyr Asn Asn Gln Leu Asp

1010 1015 1020

Asn Lys Gln Thr Asn Leu Met Leu Pro Glu Ser Thr Val Tyr Gly Asp

1025 1030 1035 1040

Val Asp Leu Ser Asn Lys Ile Asn Glu Met Lys Thr Phe Asn Ser Pro

1045 1050 1055

Asn Leu Lys Asp Gly Arg Phe Val Asn Pro Ser Gly Gln Pro Thr Pro

1060 1065 1070

Tyr Ala Thr Thr Gln Leu Ile Gln Ser Asn Leu Ser Asn Asn Met Asn

1075 1080 1085

Asn Gly Ser Gly Asp Ser Gly Glu Lys His Trp Lys Pro Leu Gly Gln

1090 1095 1100

Gln Lys Gln Glu Val Ala Pro Val Gln Tyr Asn Ile Val Glu Gln Asn

1105 1110 1115 1120

Lys Leu Asn Lys Asp Tyr Arg Ala Asn Asp Thr Val Pro Pro Thr Ile

1125 1130 1135

Pro Tyr Asn Gln Ser Tyr Asp Gln Asn Thr Gly Gly Ser Tyr Asn Ser

1140 1145 1150

Ser Asp Arg Gly Ser Ser Thr Ser Gly Ser Gln Gly His Lys Lys Gly

1155 1160 1165

Ala Arg Thr Pro Lys Val Pro Lys Gln Gly Gly Met Asn Trp Ala Asp

1170 1175 1180

Leu Leu Pro Pro Pro Pro Ala His Pro Pro Pro His Ser Asn Ser Glu

1185 1190 1195 1200

Glu Tyr Asn Ile Ser Val Asp Glu Ser Tyr Asp Gln Glu Met Pro Cys

1205 1210 1215

Pro Val Pro Pro Ala Arg Met Tyr Leu Gln Gln Asp Glu Leu Glu Glu

1220 1225 1230

Glu Glu Asp Glu Arg Gly Pro Thr Pro Pro Val Arg Gly Ala Ala Ser

1235 1240 1245

Ser Pro Ala Ala Val Ser Tyr Ser His Gln Ser Thr Ala Thr Leu Thr

1250 1255 1260

Pro Ser Pro Gln Glu Glu Leu Gln Pro Met Leu Gln Asp Cys Pro Glu

1265 1270 1275 1280

Glu Thr Gly His Met Gln His Gln Pro Asp Arg Arg Arg Gln Pro Val

1285 1290 1295

Ser Pro Pro Pro Pro Pro Arg Pro Ile Ser Pro Pro His Thr Tyr Gly

1300 1305 1310

Tyr Ile Ser Gly Pro Leu Val Ser Asp Met Asp Thr Asp Ala Pro Glu

1315 1320 1325

Glu Glu Glu Asp Glu Ala Asp Met Glu Val Ala Lys Met Gln Thr Arg

1330 1335 1340

Arg Leu Leu Leu Arg Gly Leu Glu Gln Thr Pro Ala Ser Ser Val Gly

1345 1350 1355 1360

Asp Leu Glu Ser Ser Val Thr Gly Ser Met Ile Asn Gly Trp Gly Ser

1365 1370 1375

Ala Ser Glu Glu Asp Asn Ile Ser Ser Gly Arg Ser Ser Val Ser Ser

1380 1385 1390

Ser Asp Gly Ser Phe Phe Thr Asp Ala Asp Phe Ala Gln Ala Val Ala

1395 1400 1405

Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln Met Gln

1410 1415 1420

Asp Ala Ala Gly Arg Arg His Phe His Ala Ser Gln Cys Pro Arg Pro

1425 1430 1435 1440

Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser Ala Ala Val Met Gln

1445 1450 1455

Lys Thr Arg Pro Ala Lys Lys Leu Lys His Gln Pro Gly His Leu Arg

1460 1465 1470

Arg Glu Thr Tyr Thr Asp Asp Leu Pro Pro Pro Pro Val Pro Pro Pro

1475 1480 1485

Ala Ile Lys Ser Pro Thr Ala Gln Ser Lys Thr Gln Leu Glu Val Arg

1490 1495 1500

Pro Val Val Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr Asp Arg

1505 1510 1515 1520

Ser Ser Asp Arg Lys Gly Ser Ser Tyr Lys Gly Arg Glu Val Leu Asp

1525 1530 1535

Gly Arg Gln Val Val Asp Met Arg Thr Asn Pro Gly Asp Pro Arg Glu

1540 1545 1550

Ala Gln Glu Gln Gln Asn Asp Gly Lys Gly Arg Gly Asn Lys Ala Ala

1555 1560 1565

Lys Arg Asp Leu Pro Pro Ala Lys Thr His Leu Ile Gln Glu Asp Ile

```
    1570                1575                1580
Leu Pro Tyr Cys Arg Pro Thr Phe Pro Thr Ser Asn Asn Pro Arg Asp
1585                1590                1595                1600
Pro Ser Ser Ser Ser Ser Met Ser Ser Arg Gly Ser Gly Ser Arg Gln
                1605                1610                1615
Arg Glu Gln Ala Asn Val Gly Arg Arg Asn Ile Ala Glu Met Gln Val
            1620                1625                1630
Leu Gly Gly Tyr Glu Arg Gly Glu Asp Asn Asn Glu Glu Leu Glu Glu
        1635                1640                1645
Thr Glu Ser
    1650
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 855..1187

(D) OTHER INFORMATION: /note= "N signifies gap in sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
CAGATTGTTG CTCAAGGTCG AACAGTGACA TTTCCCTGTG AAACTAAAGG AAACCCACAG      60
CCAGCTGTTT TTTGGCAGAA AGAAGGCAGC CAGAACCTAC TTTTCCCAAA CCAACCCCAG     120
CAGCCCAACA GTAGATGCTC AGTGTCACCA ACTGGAGACC TCACAATCAC CAACATTCAA     180
CGTTCCGACG CGGGTTACTA CATCTGCCAG GCTTTAACTG TGGCAGGAAG CATTTTAGCA     240
AAAGCTCAAC TGGAGGTTAC TGATGTTTTG ACAGATAGAC CTCCACCTAT AATTCTACAA     300
GGCCCAGCCA ACCAAACGCT GGCAGTGGAT GGTACAGCGT TACTGAAATG TAAAGCCACT     360
GGTGATCCTC TTCCTGTAAT TAGCTGGTTA AAGGAGGGAT TTACTTTTCC GGGTAGAGAT     420
CCAAGAGCAA CAATTCAAGA GCAAGGCACA CTGCAGATTA AGAATTTACG GATTTCTGAT     480
ACTGGCACTT ATACTTGTGT GGCTACAAGT TCAAGTGGAG AGGCTTCCTG GAGTGCAGTG     540
CTGGATGTGA CAGAGTCTGG AGCAACAATC AGTAAAAACT ATGATTTAAG TGACCTGCCA     600
GGGCCACCAT CCAAACCGCA AGTCACTGAT GTTACTAAGA ACAGTGTCAC CTTGTCCTGG     660
CAGCCAGGTA CCCCTGGAAC CCTTCCAGCA AGTGCATATA TCATTGAGGC TTTCAGCCAA     720
TCAGTGAGCA ACAGCTGGCA GACCGTGGCA AACCATGTAA AGACCACCCT CTATACTGTA     780
AGAGGACTGC GGCCCAATAC AATCTACTTA TTCATGGTCA GAGCGATCAA CCCCAAGGTY     840
```

TCAGTGACCC AAGTNAAACC ACAGAAAAAC AATGGATCCA CTTGGGCCAA TGTCCCTCTA 900

CCTCCCCCCC CAGTCCAGCC CCTTCCTGGC ACGGAGCTGG AACACTATGC AGTGGAACAA 960

CAAGAAAATG GCTATGACAG TGATAGCTGG TGCCCACCAT TGCCAGTACA AACTTACTTA 1020

CACCAAGGTC TGGAAGATGA ACTGGAAGAA GATGATGATA GGGTCCCAAC ACCTCCTGTT 1080

CGAGGCGTGG CTTCTTCTCC TGCTATCTCC TTTGGACAGC AGTCCACTGC AACTCTTACT 1140

CCATCCCCAC GGGAAGAGAT GCAACCCATG CTGCAGGCTT CACCTNTTTA CCTCCTCTCA 1200

AAGACCTCGA CCTACCAGCC CATTTTCTAC TGACAGTAAC ACCAGTGCAG CCCTGAGTCA 1260

AAGTCAGAGG CCTCGGCCCA CTAAAAAACA CAAGGGAGGG 1300

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 434 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 285..396

(D) OTHER INFORMATION: /note= "Xaa signifies gap in sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Ile Val Ala Gln Gly Arg Thr Val Thr Phe Pro Cys Glu Thr Lys
1 5 10 15

Gly Asn Pro Gln Pro Ala Val Phe Trp Gln Lys Glu Gly Ser Gln Asn
20 25 30

Leu Leu Phe Pro Asn Gln Pro Gln Gln Pro Asn Ser Arg Cys Ser Val
35 40 45

Ser Pro Thr Gly Asp Leu Thr Ile Thr Asn Ile Gln Arg Ser Asp Ala
50 55 60

Gly Tyr Tyr Ile Cys Gln Ala Leu Thr Val Ala Gly Ser Ile Leu Ala
65 70 75 80

Lys Ala Gln Leu Glu Val Thr Asp Val Leu Thr Asp Arg Pro Pro Pro
85 90 95

Ile Ile Leu Gln Gly Pro Ala Asn Gln Thr Leu Ala Val Asp Gly Thr
100 105 110

Ala Leu Leu Lys Cys Lys Ala Thr Gly Asp Pro Leu Pro Val Ile Ser
115 120 125

Trp Leu Lys Glu Gly Phe Thr Phe Pro Gly Arg Asp Pro Arg Ala Thr

130 135 140

Ile Gln Glu Gln Gly Thr Leu Gln Ile Lys Asn Leu Arg Ile Ser Asp
145 150 155 160

Thr Gly Thr Tyr Thr Cys Val Ala Thr Ser Ser Ser Gly Glu Ala Ser
165 170 175

Trp Ser Ala Val Leu Asp Val Thr Glu Ser Gly Ala Thr Ile Ser Lys
180 185 190

Asn Tyr Asp Leu Ser Asp Leu Pro Gly Pro Pro Ser Lys Pro Gln Val
195 200 205

Thr Asp Val Thr Lys Asn Ser Val Thr Leu Ser Trp Gln Pro Gly Thr
210 215 220

Pro Gly Thr Leu Pro Ala Ser Ala Tyr Ile Ile Glu Ala Phe Ser Gln
225 230 235 240

Ser Val Ser Asn Ser Trp Gln Thr Val Ala Asn His Val Lys Thr Thr
245 250 255

Leu Tyr Thr Val Arg Gly Leu Arg Pro Asn Thr Ile Tyr Leu Phe Met
260 265 270

Val Arg Ala Ile Asn Pro Lys Val Ser Val Thr Gln Xaa Lys Pro Gln
275 280 285

Lys Asn Asn Gly Ser Thr Trp Ala Asn Val Pro Leu Pro Pro Pro Pro
290 295 300

Val Gln Pro Leu Pro Gly Thr Glu Leu Glu His Tyr Ala Val Glu Gln
305 310 315 320

Gln Glu Asn Gly Tyr Asp Ser Asp Ser Trp Cys Pro Pro Leu Pro Val
325 330 335

Gln Thr Tyr Leu His Gln Gly Leu Glu Asp Glu Leu Glu Glu Asp Asp
340 345 350

Asp Arg Val Pro Thr Pro Pro Val Arg Gly Val Ala Ser Ser Pro Ala
355 360 365

Ile Ser Phe Gly Gln Gln Ser Thr Ala Thr Leu Thr Pro Ser Pro Arg
370 375 380

Glu Glu Met Gln Pro Met Leu Gln Ala Ser Pro Xaa Phe Thr Ser Ser
385 390 395 400

Gln Arg Pro Arg Pro Thr Ser Pro Phe Ser Thr Asp Ser Asn Thr Ser
405 410 415

Ala Ala Leu Ser Gln Ser Gln Arg Pro Arg Pro Thr Lys Lys His Lys
420 425 430

Gly Gly

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 444 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
GCCCAGGCAG TTGCTGCAGC TGCGGAGTAT GCGGGCCTGA AAGTGGCTCG CCGCCAAATG      60
CAAGATGCTG CTGGCCGCCG CCACTTCCAT GCCTCTCAGT GCCCAAGGCC CACGAGTCCT     120
GTGTCCACAG ACAGCAACAT GAGTGCTGTT GTGATCCAGA AAGCCAGACC CGCCAAGAAG     180
CAGAAACACC AGCCAGGACA TCTGCGCAGG GAAGCCTACG CAGATGATCT TCCACCCCCT     240
CCAGTGCCAC CACCTGCTAT AAAATCGCCC ACTGTCCAGT CCAAGGCACA GCTGGAGGTA     300
CGGCCTGTCA TGGTGCCAAA ACTCGCGTCT ATAGAAGCAA GGACAGATAG ATCGTCAGAC     360
AGAAAAGGAG GCAGTTACAA GGGGAGAGAA GCTCTGGATG GAAGACAAGT CACTGACCTG     420
CGAACAAATC CAAGTGACCC CAGA                                            444
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Ala Gln Ala Val Ala Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala
1               5                  10                  15
Arg Arg Gln Met Gln Asp Ala Ala Gly Arg Arg His Phe His Ala Ser
            20                  25                  30
Gln Cys Pro Arg Pro Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser
        35                  40                  45
Ala Val Val Ile Gln Lys Ala Arg Pro Ala Lys Lys Gln Lys His Gln
    50                  55                  60
Pro Gly His Leu Arg Arg Glu Ala Tyr Ala Asp Asp Leu Pro Pro Pro
65                  70                  75                  80
Pro Val Pro Pro Pro Ala Ile Lys Ser Pro Thr Val Gln Ser Lys Ala
                85                  90                  95
```

Gln Leu Glu Val Arg Pro Val Met Val Pro Lys Leu Ala Ser Ile Glu

100 105 110

Ala Arg Thr Asp Arg Ser Ser Asp Arg Lys Gly Gly Ser Tyr Lys Gly

115 120 125

Arg Glu Ala Leu Asp Gly Arg Gln Val Thr Asp Leu Arg Thr Asn Pro

130 135 140

Ser Asp Pro Arg

145